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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                   Score
                                            70.5
70.5
70.5
70.5
                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                          100.0
                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASTKLFFSVITVMMLIAMA......FGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-882-434A-1
551
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:+
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:+
                                                                                                                                                                                                                                                                                                                                                                       Length DB
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                                                1280
1283
267
267
267
267
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                                                                       AAW31738
AAB10456
AAB81064
AAB81065
AAB896121
AAM95431
AAW17599
       AAW34998
AAU50762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Search time 66 Seconds (without alignments) 205.933 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908470
                                                               Cynomologous monke
Human testicular a
Human reproductive
Novel signal trans
                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                             Macadamia integrif
S. pastorianus mut
Cynomologous monke
Archaebacterium AE
Propionibacterium
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ALIGNMENTS

RESULT 1 AAW31738 ID AAW3

AAW31738 standard; Protein; 102 AA.

Macadamia integrifolia antimicrobial protein 1.

Antimicrobial protein 1; growth inhibition; fungus; bacterium;

27-MAR-1998 (first entry)

AAW31738;

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Goulter KC,
                                                31-JAN-1997;
                                                                07-AUG-1997.
                                                                                                                              Key
                                31-JAN-1996;
                                                                             WO9728185-A1
                                                                                                     Peptide
                                                                                                                     Peptide
                                                                                                                                           Macadamia integrifolia.
              (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
                                                                                                                                                          fungi; bacteria; pathogen control.
Green JL,
                                96AU-0007802.
                                               97WO-AU00052.
                                                                                                     /label= sig_peptide
27..102
                                                                                                                            Location/Qualifiers
                                                                                            /label= mat_peptide
Harrison SJ,
Manners JM,
Marcus JP;
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Dog P-glycoprotein

Length 486;

DB 21;

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Query Match
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                             65
                              Matches
                                                                                                                                                                                                           RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant hexokinase, useful for the detection of creatinine kinase and glucose, comprises a deletion, addition or insertion in the wild-type amino acid sequence -
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                      1 MASTKLFFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDF 60
                                                                                                                         The present sequence is Macadamia integrifolia antimicrobial protein 1, which exerts inhibitory activity on the growth of fungiand bacteria. It can be used for the control of pathogens in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexokinase; mutant; creatinine kinase detection; glucose detection.
                                                                                                                                                                                                                                                                                                       1 MASTKLFFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDF
                                                             inhibiting the growth of fungi and bacteria in plants and animals
                                                anti-microbial protein from Macadamia integrifolia - active
                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                           Length 102;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                        SYTGOTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                                                                                                                                                                        SYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                         100.0%; Score 551; DB 18;
100.0%; Pred. No. 1.5e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pastorianus mutant hexokinase protein.
                                                                                                Claim 1; Pages 23-24; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB10456 standard; Protein; 486 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 8-9; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0359018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0359018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces pastorianus
                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-501189/45.
     WPI; 1997-448317/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                  102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA71483.
                       N-PSDB; AAT88851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2000175688-A.
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                                                                                                                                                                                animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB10456;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 VFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                  369 FGINTTVOERKLIRRLSELIGA------RAARLSVCGIAAVCOKRGYK---TG 412
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                        FSVITVMM----LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a polynucleotide sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                          27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                              413 HIAA-----DGSVYNRYPGFKEKAANALKDIYGW 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cynomologous monkey P-glycoprotein variant 1.
                                                                                                                                                                                                                                                    OTAALYNOAGCSGVAHTRF-GSSARACNP----FGW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 71; DB 25.5%; Pred. No. 42; Live 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crespi CL;
                                                          10; Mismatches
13.5%; Score 74.5; 29.2%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB81064 standard; Protein; 1280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 57-59; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steimel-Crespi DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26592.
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                          Local Similaricy
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENT-) GENTEST CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200123565-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stocker PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  efflux pump.
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                                                                Matches
                                                                                Best
                                                                                             Query Match
                                                                                                                                             This invention relates to a polynucleotide sequence encoding a cynomologous monkey P-glycoprotein (PGP), and an allelic variant of the PGP protein. PGP, also known as multidrug transporter, MDR1 is a member of the ABC transporter superfamily. The enzyme serves as an efflux pump exporting small molecules across the cell membrane. The invention includes a cynomologous monkey (Macaca fascicularis) PGP coding sequence and protein, and also that of an allelic variant. The PGP polynucleotide sequence is useful for increasing PGP transporter activity in a cell. Antisense sequences of the CDNA are useful for inhibiting PGP transport activity in a mammalian cell. They may also be used for increasing the bloavailability of a drug. The present sequence represents the cynomologous monkey P-glycoprotein variant 2. The protein has an additional 3 amino acids when compared to PGP variant 1 (AABB1065).
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 65-68; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1999;
12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             key Location/Qualifiers Misc-difference 93..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cynomologous efflux pump.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stocker PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-2000; 2000WO-US26592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENT-) GENTEST CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-2001
337 VFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
                                                                              Local
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                            6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHOKGGYD 59
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DB; AAF86128.
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                                                                             Similarity
                                                                                                                       1283 AA;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steimel-Crespi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monkey P-glycoprotein variant
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99US-0158818.
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to PGP variant AAB81064"
                                                                           12.9%;
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                                                                          Score 71; DB
Pred. No. 42;
                                                           Mismatches
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'
                                                                                      Length 1283;
                                                           Indels
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ABB96121
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                                                                               14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
                                 01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                     14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene thorapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2000;
17-MAR-2000;
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              2000US-0229287.
2000US-0229343.
2000US-0229344.
2000US-0229345.
2000US-0229345.
2000US-0229513.
2000US-0230437.
                                                                                 2000US-0227182.
2000US-0227009.
2000US-0228924.
                                                                                                           2000US-0225268
2000US-0225447
2000US-0225447
2000US-0225475
2000US-0225757
2000US-0225758
2000US-0225759
2000US-0226681
2000US-0226681
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2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225267.
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2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-0220963.

2000US-0220964.
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2000US-0215135.
2000US-0216647.
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2000US-0186350.
2000US-0189874.
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2000US-0209467
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2000US-0236370.
2000US-0236602.
2000US-0237037.
2000US-0237038.
2000US-0237039.
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2000US-0246478.
2000US-0246523.
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2000US-0246525.
2000US-0246526.
2000US-0246526.
                                 2000US-0232081.
2000US-0231968.
2000US-0232397.
                                                                                                           21-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234998.
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27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235836.
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2000US-0249244.
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29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
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                                                                                                     2000US-0234223
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                           2000US-0232080
                                                      2000US-0232398
                                                                          2000US-0232401
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
114-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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08-NOV-2000;
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Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AFTVWSGPGCNNRAERYSKCGCSAIHOKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87
                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 1505; 766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM95431 standard; Protein; 267 AA
                                                                                                                                                                                                                                                                                                    Rosen CA, Barash SC, Ruben SM;
                                    17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251868.
06-DEC-2000; 2000US-0251868.
                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251989.

08-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0254097.

05-JAN-2001; 2001US-0259678.
          17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 FGGSSSGSSGFKSV 217
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Matches 20; Conserval
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                                                                                                                                                                                                                                                                                                                               WPI; 2001-483232/52
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AAM95431
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17-JAN-2001; 2001WO-US01339.

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31-JAN-2000
24-FEB-2000)
22-FEB-2000)
11-MAR-2000)
11-MAR-2000)
11-MAR-2000)
11-JUL-2000)
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11-SEP-2000]
2000US-0179065.
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2000US-0184664.
2000US-0198173.
2000US-0199874.
2000US-0219807.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-0214886.
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2000US-021488.
2000US-021489.
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2000US-0225913.
2000US-0239141.
2000US-0239141.
2000US-0239141.
2000US-0231143.
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2000US-0231144.
2000US-023149.
2000US-023149.
2000US-02334997.
2000US-02314997.
2000US-0231636.
 02-OCT-2000)
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13-OCT-2000)
20-OCT-2000)
20-OCT-2000)
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08-NOV-2000)
17-NOV-2000)
17-NO
                                                                               Rosen
                                WPI; 2001-465570/50.
N-PSDB; AAL01401.
 Isolated
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                                                                                                              HUMAN
 nucleic acid
                                                                               Barash
                                                                                                                                           2000US-02376802.
2000US-02377039.
2000US-02377039.
2000US-02377039.
2000US-02349950.
2000US-0241785.
2000US-0241785.
2000US-0241786.
2000US-0241786.
2000US-0241826.
2000US-02446178.
2000US-0246477.
2000US-0246477.
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2000US-0246477.
2000US-0246613.
2000US-0246528.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0249217.
2000US-0249218.
2000US-0251868.
2000US-0251868.
2000US-0251988.
2000US-02531989.
2000US-02531989.
                                                                                                              GENOME
                                                                               SC,
                                                                                                              SCI
molecule encoding
                                                                                 Ruben
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a reproductive system antigen
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                                      The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                           Gaps
                                                                                                                                                28 AFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87
 is used in preventing, treating or ameliorating a medical condition
                                                                                                                             5;
                                                                                                         . Match 12.8%; Score 70.5; DB 22; Length 267; Local Similarity 27.0%; Pred. No. 7.9; es 20; Conservative 13; Mismatches 36; Indels 5,
                   Claim 11; SEQ ID NO 4089; 1297pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                    Novel signal transduction pathway protein, Seg ID 1164.
                                                                                                                                                                                                                                                         AAU17599 standard; Protein; 267 AA
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04-FEB-2000, 2000US-0186628.
24-FEB-2000, 2000US-018664.
02-MAR-2000, 2000US-0186350.
16-MAR-2000, 2000US-0199076.
17-MAR-2000, 2000US-019076.
18-APR-2000, 2000US-019123.
19-MAY-2000, 2000US-029467.
28-JUN-2000, 2000US-0214886.
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                                                                                     267 AA
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                                                                                      Sequence
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                                                                                                         Query Match
                                                                                                                             Matches
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AAU17599
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2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246477.
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2000US-0231242,
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2000US-0244617.
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14-AUG-2000;
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N-PSDB;
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                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                  AAS27516.
                                                                                              SEQ ID No 1164; 880pp; English
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2000US-0249216.
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2000US-0249208.
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immudisorders and neuronal disorders -

The invention relates to novel isolated polypeptides (I), and CD polynucleotides (II), (II) and the antibody to (I) are useful for CD disgnosting, preventing and treating diseases including immune system CD disorders (e.g. congenital and acquired immunodeficiencies, autoimmune CD transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and CD ther blood-related disorders (sickle cell anaemia), myeloproliferative CD disorders (e.g. Gaucher's disease and cancer), neurodegenerative CD disorders (e.g. Gaucher's disease and cancer), neurodegenerative CD disorders (e.g. Alzheimer's disease, parkinson's disease), chromosomal CD abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal CD disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in conditions and cell proliferation, endocrine disorders (e.g. arthythmia), respiratory disorders, dermatological disorders (e.g. arthythmia), respiratory disorders (e.g. arthythmia) (e.g. arthythm Addison's disease), reproductive system disorders, gastrointestinal

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AAW34998
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                                      This protein comprises an endoglucanase of archaebacterium AEPIIIa (Clone 63GP1), a hydrothermal vent isolate. The endoglucanase is capable of degrading carboxymethylcellulose and of hydrolysing the beta-1,4-glycosidic bonds in cellulose. It has homology to another endoglucanase (see AAW34985) of archaebacterium AEPIIIa. It can be produced from native cells or from recombinant host cells, especially prokaryotic host cells transformed with a plasmid or virus-derived vector including the endoglucanase DNA (see AAW34906). 24 Endoglucanases (see AAW34986-W35008) are claimed. They can be used to degrade cellulose for the conversion of plant biomass into fuels and chemicals, for use in detergents, textiles, animal feed, waste treatment, and in the fruit juice and brewing industries for the conversion and brewing industries for
                               the clarification and extraction of
                                                                                                                                                                                                                                                                 Claim 1; Fig 1N; 164pp; English.
                                                                                                                                                                                                                                                                                                  beta-1,4-glycosidic bonds in cellulose
                                                                                                                                                                                                                                                                                                                    Endoglucanase(s), useful to degrade
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT94206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-018435/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaebacterium isolate AEPPII1a (Clone 63GP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biomass; beta-1,4-glycosidic bond; hydrolysis; thermostable enzyme; thermophilic; glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                        Lam DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaebacterium AEPIIla endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW34998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder (inflammatory disorders), liver disorders (cirrhosis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RECO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFEFWDSPFNSDRGGRGH--GLRGAFSAGFGEFPAFMEAFSSFNMLGCSGGSHTTFSSTS 201
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mathur EJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0651572
                                                                                                                                                                                                                                                                                                                preferably form archael bacterium, AEPII la carboxymethylcellulose and hydrolyse of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.8%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by the across. The disorders include SAPHO syndrome (synovitis, cane by pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. across is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. across in a patient comprises contacting the presence or absence of P. across in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies appecific for P. across proteins. These antibodies can be used to downregulate expression and activity of P. across polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                123 IPEWYEAGISAIWIPPASKGMSGGYSMGYDPYDFFDLGE----YNO---KGTIETRFGSK 175
                                                                                                                                                                                                                                                                                41 AERYSKCGCSAI-----HOKGG-----YDFSYTGOTAALYNQAGCSGVAHTRFGSS 86
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                                                                     43;
   DB 19; Length 524;
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                                                                  37; Indels
                                                                                                                                        3 STKLFFSV-ITVMMLIAMA-----SEMVNGSAFT---VWSGPG---
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rter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; osteopathic; neuroprotectant.
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12.8%; Score 70.5; Dl
26.4%; Pred. No. 17;
:ive 12; Mismatches
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J, Zhang Y, Jen S, Carter
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                         33; Conservative
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   Query Match
Best Local Similarity
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therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enryme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
                                                                                                                                                                                                                                              14 MMLIAMASEMVNGSAFTVW-SGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQ 72
                                                                                                                                                                                                                                                                                   53 LMLIRLPRESVQ-----WPSGPASIFRA---SCGTST-----TASTSAAW-V 90
                                                                                                                                                                                                             30;
                                                                                                                                                                    12.5%; Score 69; DB 22; Length 138; 31.5%; Pred. No. 5.4; ive 8; Mismatches 25; Indels 3
                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crespi CL;
                                                                                                                                                                                                                                                                                                                                                           91 GSCSRIEHTAGAAASSPRISSRLASP-GWKSI 121
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                                                                                                                                                                                                                                                                                                                          73 AGCSGVAHTRFGS-----SARACNPFGWKSI
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                                                                                                                                                                  Query Match
Best Local Similarity 31.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 log P-glycoprotein SEQ ID 7.
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                                                                                                                                   138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-2001
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                                                                                                                                       Sequence
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1280 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                 Query Match
Best Local (
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                              The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP 'knockout' phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for human Aleanaca
                                                                                                     The present sequence is dog P-glycoprotein (PGP). The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC
                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 72-75; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    New dog P-glycoproteins (PGP) and their encoding for determining the bioavailability of drugs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235373/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stocker PJ, Steimel-crespi DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dog; P-glycoprotein; PGP; multidrug transporter; MDR1; drug bioavailability; transgenic animal; genetic model
                                                                                                                                                        human diseases.
                                                                                                                                                                                                                                                                                                                                                                                                          PGP inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dog P-glycoprotein (PGP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE00304 standard; Protein; 1280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 VFFSVLIGAFSIGOASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 -----FSY------TGOTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LFFSVITVMMLJAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
    L Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD03489
                                                               1280 AA;
    Conservative
                                                                                            family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0156510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%;
                12.5%; Score 69; DB 25.5%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB Pred. No. 70;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crespi CL,
                             DB 22; Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids, useful for screening for dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patten
28;
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33;

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336 VFFSVLIGAFSIGOASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59

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PH XXX PR XXX PR
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          Matches
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP (knockout, phenotype. They are used to propaga a non-human pGP inhibitors.)
                                                                                                                                                                                         as genotype C protein. The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC transporter family.
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                            The present sequence is dog P-glycoprotein (PGP) also referred
                                                                                                                                                                                                                                                                                                                                         numan
                                                                                                                                                                                                                                                                                                                                                             transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 64-66; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stocker PJ, Steimel-crespi DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-235373/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE00303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE00303 standard; Protein; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENT-) GENTEST CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 VFFSVLIGAFSIGOASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ----FSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
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                                                                                                                                                                                                                                                                                                                                     diseases
          25,
                                     Similarity
                                                                                                                                     1281 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                              12.5%;
      12;
                              Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TGOTAALYNQAGC
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crespi CL,
                              70;
   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reif TC,
                                                                 Length 1281;
Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patten
Gaps
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New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is dog P-glycoprotein (PGP) allelic variant. This sequence is also referred as Genotype A protein. The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patten CJ;
                                                                                                                                                                                                                                                    Dog; P-glycoprotein allelic variant; PGP; multidrug transporter;
MDR1; drug bioavailability; transgenic animal; genetic model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 69; DB 22; Length 1281; 25.5%; Pred. No. 70; tive 12; Mismatches 33; Indels 28
                                                                                                                                                                                                                                                                                                                                                                       /note= "His of GenotypeC substituted by Gln"
                                                                                                                                                                                                                     Dog P-glycoprotein (PGP) allelic variant (Genotype A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reif TC,
                               396 FKNVHFSYPSRKEVKILKGLNLKVQSĠQŤVALVGNSĠĆ 433
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crespi CL,
 ------TGQTAALYNQAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 91-93; 111pp; English.
                                                                                                                                                                                                                                                                                                                              ney
Misc-difference 197
                                                                                                                      AAE00308 standard; Protein; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stocker PJ, Steimel-crespi DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                       (first entry)
 60 ----FSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENT-) GENTEST CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-235373/24.
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Matches 25, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transporter family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD03504.
                                                                                                                                                                                                                                                                                                         Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human diseases.
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                                                                                                                                                         AAE00308;
                                                                                      RESULT 13
                                                                                                       AAE00308
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New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are used as oligonucleotide probes. Complements of PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP 'knockout' phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is dog P-glycoprotein (PGP) allelic variant. This sequence is also referred as Genotype B protein. The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patten CJ;
                                                                                                                                                                                                                                                                                                      Dog, P-glycoprotein allelic variant, PGP, multidrug transporter, MDR1, drug bioavailability, transgenic animal, genetic model.
                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Asn of GenotypeC substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "His of GenotypeC substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reif TC,
                                                                                                                                                                                                                                                                  Dog P-glycoprotein (PGP) allelic variant (Genotype B)
                                                                    396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crespi CL,
                                      ----FSY----TGQTAALYNQAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 99-102; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
Misc-difference 25
                                                                                                                                                               AAE00309 standard; Protein; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stocker PJ, Steimel-crespi DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 197
                                                                                                                                                                                                                                                                                                                                                         Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB, AAD03505
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Query Match 12.5%; Score 69; DB 22; Length 1281; Best Local Similarity 25.5%; Pred. No. 70; Matches 25; Conservative 12; Mismatches 33; Indels 21

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Gaps

28;

6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59

Conservative

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RESULT 15
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                                                                                                                                    The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for creening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP (knockout, phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New dog P-glycoproteins (PGP) and their encoding for determining the bioavailability of drugs and PGP inhibitors -
                        human diseases.
The present sequence is dog P-glycoprotein (PGP) allelic variant.
This sequence is also referred as Genotype D protein. The PGP
enzyme functions as an efflux pump exporting small molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 108-110; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235373/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US26767
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   is a member of
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for screening for
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  396
                                                  336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395
                           60
                                                                          6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC
                           ----FSY-----TGQTAALYNQAGC
                                                                                                                                                    1281 AA;
                                                                                                   Conservative
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                                                                                                   12; Mismatches
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Pred. No. 70;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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551
1 MASTKLFFSVITVMMLIAMA......FGSSARACNPFGWKSIFIQC 102
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120.046 Million cell updates/sec
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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    US-07-872-678A-48
US-08-583-276-19
US-08-752-447-2
US-09-316-167-2
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US-08-596-014A-4
US-08-596-014A-2
US-08-596-014A-2
US-08-897-620-4
US-08-877-620-2
US-08-878-620-2
US-08-93-1
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Sequence 48, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 105, Appli Sequence 107, Appli Sequence 97, Appli Sequence 97, Appli Sequence 107, Appli Sequence 108, Appli Sequence 108, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 25, Appli Sequence 27, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 21, Appli Sequen
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391 RAARLSVCGIAAICOKRGYK---TGHIAA-----DGSVSTRYPGFKEKAANALKDIYG 440 40 RAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRF-GSSARACNP----FG Query Match Best Local Similarity 39.3 Matches 24; Conservative

13.5%;

Score 74.5; DI Pred. No. 1.1; Mismatches

DB 1; 18;

Length 486; Indels 15;

Gaps 94

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RESULT 1 US-07-872-678A-48 US-07-872-678A-48 US-07-872-678A-48 Sequence 48, Application US/07872678A Patent No. 5541060 GENERAL INFORMATION: APPLICANT: Bell, Graeme, et al. TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELI UNDERS OF EXQUENCES: 48 CORRESPONDENCE ADDRESS: 48 CORRESPONDENCE ADDRESS: 48 CORPUTER: USA ZIP: 77210 COMPUTER: Texas COUNTRY: USA ZIP: 77210 COMPUTER: READABLE FORM: MEDLIUM TYRE: Floppy disk COMPUTER: BRECHIN Release #1.0, Version #1.25 OPERATION SYSTEM: PC-DOS/MS-DOS OPERATION SYSTEM: PC-DOS/MS-DOS OPERATION SYSTEM: PC-DOS/MS-DOS OPERATION NUMBER: US/07/872,678A FILING DATE: 22-APRIL-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: COUGhlin, Daniel F. REGISTRATION NUMBER: 36,111 REFERENCE/DOCKET NUMBER: ARCDO16 TELEPAN: 713-789-2679 TELECOMMUNICATION INFORMATION: TELEPHONE: 713-789-2679 TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 486 amino acids TYPE: anino acids TYPE: DNA (genomic)	28 60 10.9 871 4 US-09-245-041-19 30 60 10.9 1198 4 US-09-245-041-131 31 60 10.9 1350 4 US-09-245-041-17 32 60 10.9 2787 4 US-09-245-041-17 33 59.5 10.8 305 4 US-09-245-041-17 34 59.5 10.8 861 4 US-09-260-048-12 35 59 10.7 352 2 US-08-960-048-12 36 59 10.7 352 2 US-08-960-041-9 37 59 10.7 1260 4 US-09-245-041-9 38 59 10.7 1260 4 US-09-245-041-2 39 59 10.7 1260 4 US-09-245-041-2 40 58.5 10.6 415 4 US-09-134-001C-397 41 58.5 10.6 510 4 US-09-134-001C-397 43 58.5 10.6 1404 2 US-08-97-180 45 58.5 10.6 1404 3 US-08-620-112-337 46 58.5 10.6 1404 3 US-08-611-722A-2 47 58.5 10.6 1752 4 US-09-556-877-180
ETES MELLITUS	Sequence 19, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli

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ADDALL
STREET: 300
CITY: Chicago
STATE: Illinois
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Sequence 2, Application US/08752447
Patent No. 599408
GENERAL INFORMATION:
APPLICANT: Mechetner, Eugene
APPLICANT: Mechetner, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligcal Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 VFFSVLIGAFSVGQAŠPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                    APPLICANT: Michauis, Arthur
APPLICANT: Nichhuis, Arthur
APPLICANT: Nichhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi & Stewart STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.3%; Score 68; DB Best Local Similarity 24.5%; Pred. No. 21; Matches 24; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2

COMPUTER: IBM PS/2

SOFTHOG SYSTEM: PC-DOS

SOFTHOG SYSTEM: PC-DOS

SOFTHOG SYSTEM: DW4.V2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/583,276

FILING DATE: 05-UAN-1996

CLASSIFICATION NUMBER: 07/887,712

FILING DATE: 31-OCT-1994

FILING DATE: 31-OCT-1994

FILING DATE: 22-MAY-1992

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 1280 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
                                                                                                                                                   Sequence 19, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roseland
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07068
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                                                                                                              RESULT 2
US-08-583-276-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-752-447-2
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    95 W 95
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APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Wing Immunoligcal Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||||:
334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%; Score 68; DB 2; Length 1280; 24.5%; Pred. No. 21; tive 13; Mismatches 33; Indels ;
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: McDonnell Boehnen Hulbert & Berghoff Ltd.
300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 1.05/08/752,447 FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 FRNVHFSYPSRKEVKILKGLNLKVQSGÓTVÁLVGNSGC 431
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                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5994084nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-9001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,167
                                                                                                                                     ZIP: 60606
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09316167
Patent No. 6365357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIREL. Chicago
STATE: Illinois
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Matches 24; Conserva
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US-08-701-846-2
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SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-316-167-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:4:
                                                                                                                                              Sequence 2, Application US/08701846
Patent No. 5717069
GENERAL INFORMATION:
APPLICANT: Granados, Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michael M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5206352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                               TITLE OF INVENTION: DNA SEQUENCE CODING FOR A POLYPEPTIDE TITLE OF INVENTION: WHICH ENHANCES VIRUS INFECTION OF HOST INSECTS NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 E. State St., Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/622,836 FILING DATE: 24-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
STREET: St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
                                                                                                                                                                                                                                                                                                                                                                                    334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
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                                                                                                                                                                                                                                                                                                                                                60 ----FSY-----TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                         6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ----FSY-----TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 12.3%; Score 68; DB 4; Length 1280; Local Similarity 24.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: No. 6365357nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 68; DB 6; Length 1280; 24.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
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RESULT 7
US-08-296-014A-4
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ding, Jea
APPLICANT: HO, Bow
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08296014A Patent No. 5716834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMBER: US/08/701,84
FILING DATE: 23-AUG-1996
CLASSIFICATION: 43
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/002,743
FILING DATE: 24-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A.
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-32
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (607)273-260 INFORMATION FOR SEQ ID NO:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                        ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 902 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 QYTWMNKTKR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 GGAYYGAFWTAPASTNLGEYLRVSPTNWMVIHELGHAYDFVFTVNTRLIEIWNNSFCDRI 272
                                                                                                                                                                                                                                                                              STREET: 8110 Gateno
                                                                               FILING DATE:
                                                                                           APPLICATION NUMBER: US/08/296,014A
                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AHTREGSSAR 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 902 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                            Virginia
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14850
                                                                                                                                                                                                                                                                                                  B: Birch, Stewart, Kolasch & Birch
8110 Gatehouse Road, Suite 500 East
                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/701,846
23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jeak Ling
                                                                                                                                                                                                                                                                                                                                                                     The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 67.5; D
28.6%; Pred. No. 16;
tive 10; Mismatches
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Sequence 4, Application US/08596405
Sequence 4, Application US/08596405
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 WSG--PGCNNRAERYSKCGCSAIHOKGGYDF-SYTGQTAALYNOAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                           32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.8%; Pred. No. 54;
Matches 19; Conservative 8; Mismatches 22; Indels 9;
                                                                                                                                                                                                                                               11.5%; Score 63.5; DB 1; Length 1019; 32.8%; Pred. No. 54; tive 8; Mismatches 22; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
   1781-105P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 171
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                         TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       1019 amino acids
                                                                                                                                                                                                                                                                                             19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid;
TOPOLGGY: linear;
MOLECULE TYPE: protein
                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-596-405-4
                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                         Query Match
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Sequence 2, Application US/08296014A
; Sequence 2, Application US/08296014A
; Patent No. 5716834

GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ding, Jeak Ling
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Blrch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STREET: Viginia
                                                                    GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ding, Jeak Ling
APPLICANT: Ding, Jeak Ling
APPLICANT: Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
TITLE OF SEQUENCES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query March
11.5%; Score 63.5; DB 2; Length 1019;
Best Local Similarity 32.8%; Pred. No. 54;
Matches 19; Conservative 8; Mismatches 22; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/877,620 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1781-105P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                   ; Sequence 4, Application US/08877620
; Patent No. 5985590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
US-08-877-620-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ding, Jeal
APPLICANT: HO, Bow
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08596405
Patent No. 5858706
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino acids
                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUIPPY, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/OCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 205-80
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: BILL CHURCH CITY: Falls Church CTATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                     TELLEFAX: 1.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 WSGSQPSCVKVADREVDCDSKAV-----DFLDDVGEPVRIHCPAGCSLTAGTVWGTA 429
                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murphy, Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                     22042
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XGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8110 Gatehouse Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1083 amino acide
                                                                       (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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10 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jeak Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
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Pred. No. 58;
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                                                               Matches
                                                                                           Query Match
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Matches 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ding, applicant: Ho, Bo
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             TELEFAX: 248345
378 WSGSQPSCVKVADREVDCDSKAV-----DFLDDVGEPVRIHCPAGCSLTAGTVWGTA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 WSGSOPSCVKVADREVDCDSKAV-----DFLDDVGEPVRIHCPAGCSLTAGTVWGTA 429
                                                     Local Similarity 32.8%; les 19; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS 86
                            32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                   NAME: Murphy, Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                          TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 8110 Gatehouse Road, Suite 500 Eas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
                                                                                                                                                                                          1083 amino acids
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Ho, Bow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%;
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                                                                            Score 63.5; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63.5;
Pred. No. 58;
                                                             Mismatches
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                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                             22;
                                                                                         Length 1083;
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                                                             Indels
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                                                           Gaps
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; Sequence 99, Application US/07857224B
; Patent No. 5958784

RESULT 13 US-07-857-224B-99

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5: Cutt, J. R.
5: Dixon, D. C.
5: Carr, J. P.
7: Klessig, D. F.
1solation and nucleotide sequence of CDNA clones for the pathogenesis related proteins of Nicotiniana tabacum induced by TMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ئ</u>
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31.2%; Pred. No. 5.8;
tive 5; Mismatches 24; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 SRAQNYANSRAGDCNLÍHSGAGENLAKGGGDF--TGRAAVQLWVSERPDÝNYÁTNQCVGG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 NRAERY--SKCG-CSAIHQ-----KGGYDFSYTGQTAAL-----YNQA--GCSG- 77
                                                                                                                                                                                                                            ZIP: (COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Universational post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Universational COMPUTER: Apple MacIntosh
COMPATER: Apple MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILIG DATE: 03/25/92
CLASSIFICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNONE: (International) 41 1 632 2830
              APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Lycopersicon esculentum
FEATURE: Pathogenesis related protein; Table 16 Row 3
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-347-833-11

Sequence 11, Application US/09347833

Patent No. 629468

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Odell, Joan T.

TILLE OF INVENTION: Factors Involved in Gene Expression; FILE REFERENCE: BB-1172

CURRENT APPLICATION NUMBER: US/09/347,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 --VAH-----TRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 KMCGHYTQVVWRNSVRLGCGRARCNNGWW---FISC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 31.2
Matches 30; Conservative
                                                                                                                                                                                                           COUNTRY: Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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GENERAL INFORMATION:
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                                                                                                                                                                Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 9861
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-857-224B-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: in
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                              24 VNGSAFTVWSG-PGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAH-- 80
                                                                                                                                                                                                                                                                                                                                                 14 MMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 62; DB 2; Length 3729; 28.8%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                        Query Match 11.3%; Score 62; DB 4; Length 442; Best Local Similarity 25.9%; Pred. No. 28; Matches 21; Conservative 9; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Defloff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI (DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08804227C; Patent No. 5876991; GENERAL INFORMATION:
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 GSVGAA----SAANSTRMMG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                            74 GCSGVAHTRFGSSARACNPFG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3729 amino acids
                                                                                                                                                              TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 21; Conservative
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Best Local Similarity
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US-08-804-227C-4
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                                                                                                                                          LENGTH: 442
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밁 ર્ 81 -TRFGSSARACNP 92 | | | ; | | 1 1399 WERFASAYTATRP 1411

Search completed: January 12, 2003, 09:40:11 Job time : 28 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
Published Applications AA:*

/ cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO0 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO0 PUBCOMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO0 PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 12, 2003, 09:39:30 ; Search time 20 Seconds (without alignments) 98.945 Million cell updates/sec
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551
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19	18	17	16	5	14	13	12	11	10	ဖ	æ	7	6	U	4		· N	, р	Result No.
61	64	64	64	64.5	68	89	68	69	70.5	75.5	415	417	419	421	426	426	426	551	Score
11.1	11.6	11.6	11.6	11.7	12.3	12.3	12.3	12.5	12.8	13.7	75.3	75.7	76.0	76.4	77.3	77.3	77.3	100.0	Query
501	1609	1272	1272	147	1280	1280	1280	1280	267	486	76	76	76	76	76	76	76	102	Length
8	10	10	10	9	10	10	9	9	9	10	10	10	10	10	10	10	10	10	BG
US-08-635-967-2	US-09-938-275-11	US-09-769-097-4	US-09-769-097-2	US-10-016-634A-115	US-09-866-866A-4	US-09-866-866A-2	US-10-072-621-7	US-10-044-671-2	US-09-764-868-1164	US-09-801-368-154	US-09-882-434A-20	US-09-882-434A-21	US-09-882-434A-18	US-09-882-434A-19	US-09-882-434A-17	US-09-882-434A-16	US-09-882-434A-15	US-09-882-434A-1	ID
Ap.	Sequence 11 Appl		Sequence 2, Appli	Sequence 115. App	•	е 22 ·	7		1164	154	20.	21	18,	19		16,	Sequence 15, Appl	Sequence 1, Appli	Description

45	44	43	42	41	40		38	37	36	35	34	ω u	ω N	31	30	29	28	27	26	25	24	23	22	21	2
58.5	58.5		50.	58.	58.			59	59	59	59									60.	60.5	60.		61	
10.6	10.6	10.6	10.6	10.6	•		10.7		10.8	10.8	10.8	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.1	11.1	11.1
5405	5405	1752	1431	1404	585	476	1260	549	1743	1404	861	2787	1786	1607	1350	1276	871	515	515	787	348	94	1786	1786	914
10	9	10	9	10	10	12	10	10	12	10	10	10	10	10	10	10	10	10	10	9	10	ø	10	10	9
US-09-922-217-1116	US-10-025-380-1116	US-09-841-132-180	US-09-842-930A-2	US-09-944-849-8	US-09-841-132-337	US-10-078-929-201	-09	-893		-09-862-027-2	US-09-838-539-12	6	US-09-938-275-7	US-09-938-275-10	-09	US-09-866-866A-8	US-09-893-238-19	US-09-986-552-6	US-09-895-072-6	US-09-712-363-178	US-09-791-961-2	US-09-950-933A-44	US-09-938-275-6	US-09-873-676-113	US-09-975-143-47
e 1116.	_	Sequence 180, App	Sequence 2, Appli	Sequence 8, Appli	Sequence 337, App	20	Sequence 2, Appli	9	e 451	24	12	Sequence 15, Appl	7	10				Sequence 6, Appli	w	Sequence 178, App	w	Sequence 44, Appl	Sequence 6, Appli	Sequence 113, App	Sequence 47, Appl

ALIGNMENTS

RESULT 1 US-09-882-434A-1

Sequence 1, Application US/09882434A Patent No. US20020108144A1

```
APPLICANT: Marners, John M.
APPLICANT: Marcus, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: DCT/AU97/00052
PRIOR APPLICATION NUMBER: DCT/AU97/00052
PRIOR APPLICATION NUMBER: AU DN 7802
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU DN 7802
PRIOR FILING DATE: 1996-01-31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 102
TYPE: PRT
ORGANISM: Macadamia integrifolia
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                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                         Query Match
                                                 61
61 SYTGOTAALYNOAGCSGVAHTRFGSSARACNPFGWKSIFIOC 102
                                                                                                                                                                                     . Match 100.0%; Score 551; DB 10; Local Similarity 100.0%; Pred. No. 4.1e-57; les 102; Conservative 0; Mismatches 0;
                                                                                      1 MASTKLFFSVITVMMLIAMASEMVNGSAFTVMSGPGCNNRAERVSKCGCSAIHQKGGYDF 60
                             SYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                    Length 102;
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                                                                                                                                                                                     ..
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APPLICANT: Marcus, John Paul APPLICANT: Goulter, Kenneth C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Mi28K variant. Variant MiAMP1 protein Mi28K OTHER INFORMATION: containing a Lysine at amino acid 28 (used primer OTHER INFORMATION: from SEQ ID NO:8 to produce).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 17.3%; Score 426; DB 10; Local Similarity 98.7%; Pred. No. 9.3e-43; Les 75; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCUCRATION

APPLICANT: Marners, John M.
APPLICANT: Goulter, Kenneth C.
APPLICANT: Geon, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL
PRICE REFERENCE: CULLNIS.ICPICI
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1996-11-09
SOFTWARE: FEBLESC for Windows Version 4.0
SCOFTWARE: FEBLESC for Windows Version 7.0
            US-09-882-434A-15

Sequence 15. Application US/09882434A

Patent No. US20020108144A1

GENERAL INFORMATION:

APPLICANT: Mancus, John Paul

APPLICANT: Marcus, John Paul

APPLICANT: Goulter, Kenneth C.

APPLICANT: Green, Jodie Lyn

TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN

FILE REFERENCE: CULLANIB ..PCIC.

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/364395

PRIOR APPLICATION NUMBER: 09/117615

PRIOR APPLICATION NUMBER: 09/117615

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-01-31

PRIOR FILING DATE: 1997-01-31

PRIOR FILING DATE: 1997-01-31

PRIOR FILING DATE: 1996-01-31

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FRASEEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-882-434A-16
; Sequence 16, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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-09-882-434A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 15
LENGTH: 76
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                                                                                                                                                                                                    Gaps
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; OTHER INFORMATION: Mi39K variant. Variant MiAMP1 protein Mi39K ; OTHER INFORMATION: containing a Lysine at amino acid 39 (used primer ; OTHER INFORMATION: from SEQ ID NO:9 to produce).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
                                                                                                                                             77.3%; Score 426; DB 10; Length 76; 98.7%; Pred. No. 9.3e-43; tive 1; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR PLING DATE: 1998-11-09
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1996-11-03
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FABLESEQ for Windows Version 4.0
SOFTWARE: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/0982434A
Patent No. US20020108144A1
GENERAL INFORMATION:
APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18 1CP1C1
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APPLICANT: Manners, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 76
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                    75; Conservative
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                                                                                                                                                  Query Match
Best Local Similarity
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RESULT 6
US-09-882-434A-18
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APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICOBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: 09/117615
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-01-31
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR APPLICATION NUMBER: AU PN 7802
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                                                                         ; OTHER INFORMATION: US-09-882-434A-18
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SOFTWARE: FastSEQ.for Windows Version 4.0
SEQ ID NO 19
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 76
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Best Local Similarity
                          Query Match
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PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
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CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
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TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Mi54K variant. Variant MiAMP1 protein Mi54K OTHER INFORMATION: containing a Lysine at amino acid 54 (used primer OTHER INFORMATION: from SEQ ID NO:12 to produce)
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                                                                                                                          OTHER INFORMATION: M154V variant. OTHER INFORMATION: containing a V
                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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                                                                                                Mi54V variant. Variant MiAMP1 protein Mi54V containing a Valine at amino acid 54 (used pufrom SEQ ID NO:11 to produce).
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98.7%;
  76.0%;
98.7%;
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Pred. No. 3.5e-42;
Score 419; DB 1
Pred. No. 6e-42;
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                          DB 10;
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                            Length 76
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Best Local Similarity

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GENERAL INFORMATION:
APPLICANT: Manners, John M.
APPLICANT: Mancus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
ITITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CUURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR APPLICATION NUMBER: 09/117615
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APPLICANT: Marcus, John Paul
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR APPLICATION NUMBER: 09/317615
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: NUMBER: PRIOR APPLICATION NUMBER: NUMBER: NUMBER: PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
PRIOR FILING DATE: 1996-01-31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
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Patent No. US200
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TYPE: PRT
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Similarity 97.4%;
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Pred. No. 1e-41;
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NAME/KEY: SITE
CCATION: (115)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1164
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12.5%; Score 69; DB 9; Length 1280;
Best Local Similarity 25.5%; Pred. No. 6;
Matches 25; Conservative 12; Mismatches 33; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Washington State University Research Foundation
APPLICANT: Mealey, Katrina
APPLICANT: Mealey, Katrina
APPLICANT: Mealey, Katrina
APPLICANT: Bentjen, Steven
TITLE OF INVENTION: WIRL VARIANTS AND METHODS FOR THEIR USE
FILE REFERENCE: 4630-61733
CURRENT APPLICATION NUMBER: US/10/044,671
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/21,578
PRIOR APPLICATION NUMBER: US 60/214,829
PRIOR APPLICATION NUMBER: US 60/314,829
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1164
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.8%; Score 70.5; DB 9; Length 267;
Best Local Similarity 27.0%; Pred. No. 0.66;
Matches 20; Conservative 13; Mismatches 36; Indele
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  Sequence 1164, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/10044671; Patent No. US20020177147A1; GENERAL INFORMATION:
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ORGANISM: Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 ---RACNPFGWKSI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                  US-09-764-868-1164
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US-10-044-671-2
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 69/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEC ID NOS: 440
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Mi46K/54V variant. Variant MiAMPI protein OTHER INFORMATION: Mi46K/54V containing a Lysine at amino acid 46 and OTHER INFORMATION: a Valine at amino acid 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 SAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNKAGCSGVAVTRFGSS 60
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13.7%; Score 75.5; DB 10; Length 486;
Best Local Similarity 30.2%; Pred, No. 0.35;
Matches 29; Conservative 9; Mismatches 27; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%; Score 415; DB 10; 97.4%; Pred. No. 1.8e-41; tive 1; Mismatches 1;
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Hecht, Peter
Hottzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
PRIOR FILING DATE: 1998-11-09
RIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 154, Application US/09801368
; Patent No. US20020128250A1
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ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.49
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 ARACNPEGWKSIFIOC 102
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Salama, Sofie
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US-09-882-434A-20
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                                                                                                                                                                  SEQ ID NO 20
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APPLICANT:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-621-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
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Patent No. US20020169137A1
GENERAL INFORMATION:
APPLICANT: Reiner, Peter B.
APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
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CURRENT APPLICATION NUMBER: US/10/072,621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/0986686A Patent No. US20020102244A1 GENERAL INFORMATION:
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TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sorrentino, Brian APPLICANT: Schuetz, John
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
                                                                                                  334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 39:
     60
                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                               6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1280
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                               12.3%; Score 68; DB 10; Length 1280; 24.5%; Pred. No. 7.8;
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TGQTAALYNQAGC 75
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US-10-016-634A-115
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US-09-866-866A-4
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GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
PTI.E REFERENCE: 1340-1-021CIP2
PTI.E REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115, Application US/10016634A Publication No. US20020192666A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGTH: 147
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Matches ;
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                                                                                                                                      Matches
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Recipon, Herve
APPLICANT: Ghosh, Malavika
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
FILE REFERENCE: DEX-0255
FILE REFERENCE: DEX-0255
CURRENT APPLICATION NUMBER: US/10/016,634A
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,258
PRIOR FILING DATE: 2000-10-31
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PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 176
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                Local Similarity
    84 GSSA---RACN 91
                                                                                        32 WSGPGCNNRAER-YSKCGCSAI------HQKGGYDFSYTGQTAALYNQAGCSGVAHTRF 83
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                                            5 WAGPGPAERAEEAVSGVGVEAKTQHAGQGAQPGGMGCGFSSGPIGMALGLGLVGTAATRG 64
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Pred. No. 1.7;
4; Mismatches 32;
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Db 65 GSSAWPDSTCN 75

Search completed: January 12, 2003, 09:46:46 Job time: 22 secs

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Result
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Maximum DB
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29
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seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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T22396
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T28811
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ALIGNMENTS

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probable aldehyde dehydrogenase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35804
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A;Accession: T35804
A;Accession: T35804
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-486 <COI>A;Cross-references: EMBL:X94357; NID:gl150575; PIDN:CAA64134.1; PID:gl150586
A;Cross-references: EMBL:X94357; NID:gl150575; PIDN:CAA64134.1; PID:gl150586
A;Stachelek, C.; Stachelek, J.; Swan, J.; Botstein, D.; Konigsberg, W.
Nucleic Acids Res. 14, 945-963, 1986
A;Title: Identification, cloning and sequence determination of the genes specifying hexelongues: Apage 12, 1986-1986; PMID:3003701
A;Reference number: A93649; MUID:86120382; PMID:3003701
A;Accession: B23523
A;Molecule type: DNA
A;Residues: 1-28,'I',30-60,'V',62-196,'S',198-486 <STA>
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A; Residues: 1-315 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                  hexokinase (EC 2.7.1.1) B - yeast (Saccharomyces cerevisiae)
N;Alternate names: HEX1 protein; hexokinase PII; hexokinase PII; protein G0556; protein C;Species: Saccharomyces cerevisiae
C;Date: 28-Dec-1987 #sequence revision 12-Apr-1996 #text change 16-Jun-2000
C;Accession: S61608; B23523; S22430; A23958; S05731; S33656; S64279; A53632; S28555
C;Accession: G. Hallier, E.; Robineau, S.; Netter, P.
submitted to the EMBL Data Library, December 1995
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A; Accession: S61608
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13.7%; Score 75.5; Di
Best Local Similarity 25.9%; Pred. No. 2.4;
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Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Endicott, J.A.; Sarangi, F.; Ling, V. DNA Seq. 2, 89-101, 1991
A; Title: Complete CDNA sequences encoding the Chinese hamster P-glycoprotein gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAL53581.1; PID: 917984492; GSPDB: GN00191
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C.Species: Cricetulus griseus (Chinese hamster)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C54D1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Pate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28B11
R;Minx, M.
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A,Residues: 1-1281 <RES>
A,Cross-references: GB:M60042; NID:g191168; PIDN:AAA68885.1; PID:g191169
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A;Accession: I48123
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C, Superfamily: alcohol oxidase
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                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
                              C; Accession: AB3552
                                                                                                                                                                                                                                                                                                                        A; Accession: AB3552
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R; Endicott, J.A.: S;
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A; Molecule type: DNA
A; Residues: 1-247 < GRE>
A; Accession: S33656
A; Molecule type: DNA
A; Residues: 1-247 < GRE>
A; Accession: S34656
A; Cross-references: EMBL:X67787; NID:g3707; PIDN:CAA48003.1; PID:g3710
A; Cross-references: EMBL:X67787; NID:g132930; PIDN:CAA96973.1; PID:g132931; GSPDB:GNOG
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Residues: 1-486 < CCWA
A; Rush, A; Rush, A; Vojrek, A.B.; Clifton, D.; Fraenkel, D.G.
A; Ryerismental source: strain S28C
R; Kriegel, T.W.; Rush, A; Vojrek, A.B.; Clifton, D.; Fraenkel, D.G.
B; Cross-reference number: A55632; MUID:94114477; PMID:8286332
A; Recession: A53632
A; Rocession: A53632
A; Molecule type: protein
A; Residues: 13-21 < KRI>
C; Generics:
A; Cross-references: SGD:S0003222; MIPS:YGL253W
A; Molecule type: protein
A; Residues: 13-21 < KRI>
C; Superfamily: hexokinase; hexokinase homology
C; Reywords: allosteric regulation; ATF; glycolysis; phosphoprotein; phosphotransferase
F; 2-486, Product: hexokinase benonlogy < C; Keywords: allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: hexokinase benonlogy < C, Keywords: Allosteric regulation; ATKX>
F; 36-470/Domain: ATKX>
F; 36-470/Domain: ATKX>
F; 36-470/
                                                                                                                                   A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: protein A; Molecule (1996: pr
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A;Aolecule type: protein
A;Residues: 2-12 <SCH>
R;Breitwieser, W.; Price, C.; Schuster, T.
R;Breitwieser, W.; Price, C.; Schuster, T.
A;Asat 9, 551-556, 1993
A;Title: Identification of a gene encoding a novel zinc finger protein in Saccharomyces
A;Reference number: S33654; MUID:93311123; PMID:8322518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 13.7%; Score 75.5; DB 1; Length 486; al Similarity 30.2%; Pred. No. 3.5; 29; Conservative 9; Mismatches 27; Indels 31; Gaps
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A,Cross-references: EMBL:X03483; NID:g3792; PIDN:CAA27203.1; PID:g3793
A,Note: the authors translated the codon GTT for residue 61 as Gly
A,Accession: S22430
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A;Molecule type: mRNA
A;Residues: 1-184, 'V',186-1280 <CH2>
A;Cross-references: GB:M14758; NID:g187468; PIDN:AAA59575.1; PID:g307180
A;Cross-references: GB:M14758; NID:g187468; PIDN:AAA59575.1; PID:g307180
A;Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F.
Blochem. J. 299, 309-315, 1994
A;Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase
A;Reference number: S43838; MUID:94220047; PMID:7909431
A;Accession: S43838
A;Molecule type: protein
A;Residues: 656-689 <CHA>
                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X58723; NID:g34522; PIDN:CAA41558.1; PID:g34523 R;Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I. Cell 47, 381-389, 1986 Cell 47, 381-389, 1986 A;Title: Internal duplication and homology with bacterial transport proteins in the mdrl A;Reference number: A25059; MUID:87028230; PMID:2876781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-22, 'R' <KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression A;Reference number: $15500
A;Accession: $15500
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R;Gekeler, V.; Weger, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K. submitted to the EMBL Data Library, April 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-22 < KIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multidrug resistance protein 1 - human
N;Alternate names: P-glycoprotein 1
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 18-Aug-1995 #text change 19-Jan-2001
C;Accession: A34914; PS0162; S15500; A25059; S43838; I52738; I65204
R;Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.
J. Blol. Chem. 265, 506-514, 1990
A;Tittle: Genomic organization of the human multidrug resistance (MDR1) gene and origin A;Reference number: A34914; MUID:90094448; PMID:1967175
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A;Introns: 84/3; 127/1; 166/2; 271/2; 331/1; 392/3; 433/2; 585/2; 1089/1; 1530/3
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
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A;Rolecule type: DNA
A;Residues: 1-1557 <MIN>
A;Cross-references: EMBL:U46673; PIDN:AAC48152.1; GSPDB:GN00028; CESP:C54D1.5
A;Experimental source: strain Bristol N2; clone C54D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973 ANGCQP 978
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Probst, H.
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A; Introns: 25/2; 66/1; 114/2
                                                                                                    A; Experimental source: strain Bristol N2
                                                                                                                       A;Cross-references: EMBL: U28731; NID: 9861241; PID: 9861242; PIDN: AAA68294.1; CESP: F12A10
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-184 < GEI>
                                                                                                                                                                                                                                                                                       A; Reference number: Z18451
A; Accession: T16044
                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, June 1995 A; Description: The sequence of C. elegans cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F12A10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16044
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F;994-1280/Domain: hydrophobic <HE2>
F;1053-1249/Domain: hydrophilic <HE2>
F;1053-1249/Domain: ATP-binding cassette homology <ABC2>
F;1070-1077/Region: nucleotide-binding motif A (P-loop)
F;1196-1200/Region: nucleotide-binding motif B
F;91,94,99/Binding site: carbohydrate (Asm) (covalent) #status predicted
F;433/Binding site: ATP (Lys) #status predicted
F;461,667,671/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exp
F;667,671,683/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status F;667,671,683/Binding site: phosphate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c;Superfamily: multidrug resistance protein; ATP-binding cassette homology c;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein; F;1-638,653-1280/Region: duplication F;49-350/Domain: hydrophobic <HB1> F;350/Domain: hydrophobic <HB1> F;351-637/Domain: hydrophobic <HB1> F;351-637/Domain: hydrophilic <HL1> F;410-604/Domain: ATP-binding cassette homology <ABC1> F;427-434/Region: nucleotide-binding motif A (P-loop) F;551-555/Region: nucleotide-binding motif B F;551-555/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Geisel
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A; Residues: 800-856 < RE2>
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A;Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li. A;Reference number: I52238; MUID:90290529; pMID:1972623
A;Accession: I52238
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A;Residues: 178-215 <RES>
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                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ----FSY----
                                     CESP: F12A10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 12.3%; Score 68; DB Similarity 24.5%; Pred. No. 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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Score 67.5;

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Length 184;

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C.Accession: JC6040
C.Accession: JC6040
C.Accession: JC6040
R.Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A.Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A.Reference number: JC6039; MuID:96146512; PMID:8550497
A.Accession: JC6039; MuID:96146512; PMID:8550497
A.Accession: JC6039; MuID:91184712; PIDN:AAC43598.1; PID:g1184713
A.Residues: 1.151 ccOL.
A.Cross references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A.Experimental source: strain 276755-3b
C.Genetics:
A.Gene: agfB
C.Function:
A.Description: minor component of thin aggregative fimbriae
A.Description: minor component of thin aggregative fimbriae
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A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
C;Keywords: fimbria
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-151/Froduct: fimbrin protein agfB #status predicted <MAT>
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A;Experimental source: strain IR36
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteinase inhibitor - rice

proteinase inhibitor - rice
(5,5percies: Oryza sativa (rice)
(5,5percies: Oryza sativa (rice)
(5,bate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jun-2000
(5,Accession: T02667 #., Park, J.H.; Lee, G.R.
R;Yun, C.H.; Lee, J.H.; Park, J.H.; Lee, G.R.
R;Yun, C.H.; Lee, J.H.; Park, J.H.; Lee, G.R.
A;Description: Molecular characterization of rice proteinase inhibitor gene.
A;Reference number: Z14694
A;Reference number: Z14694
A;Reference number: Z14694
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12.1%; Score 66.5; DB 2; Length 151;
Best Local Similarity 31.0%; Pred. No. 10;
Matches 18; Conservative 11; Mismatches 16; Indels 13; Gaps
                                                                                                                                                                2 ASTKLFFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYS-----KCGCSAIHQKG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MASTKLFFSVITVMMLIAMASEMVN------GSAFTVWSG------PG 36
                                     37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                                                                         138 -----GYSGYG-----GAYPGMYGGGMGGSYGSSSWGSYSSSRSG 172
                                     34; Indels
                                                                                                                                                                                                                                                                             37 CNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFG
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        9.6
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                                          11; Mismatches
        Pred. No.
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    24.18;
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                                              26, Conservative
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A,Introns: 21/1
C,Superfamily: gamma-thionin
Best Local Similarity
Matches 26; Conserve
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Matches
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geed allergen RA17 - rice
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: S21157; JC4887; S31079
R;Izumi, H.; Adachi, T.; Fujii, N.; Matsuda, T.; Nakamura, R.; Tanaka, K.; Urisu, A.; Ku;
FBES Lett. 302, 231-216, 1992
A;Title: Nucleotide sequence of a cDNA clone encoding a major allergenic protein in rice
A;Reference number: S21157; MUID:92289999; PMID:1376283
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A.Cross-references: EMBL:D11431; NID:g218194; PIDN:BAA01997.1; PID:g218195
R.Nakamura, R.; Matsuda, T.
Blosci. Blotechnol. Blotchem. 60, 1215-1221, 1996
A.fitle: Rice allergenic protein and molecular-genetic approach for hypoallergenic rice. A;Reference number: JC4887; MUID:97141195; PMID:8987539
                                                                                                                                                                                                                                                                                                                                       CjAccession: $31078
R;Adachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
Rjadachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
Ajant Mol. Biol. 21, 239-248, 1993
Ajtitle: Gene structure and expression of rice seed allergenic proteins belonging to the A;Reference number: $31078; MUID:93144699; PMID:7678765
A;Accession: $31078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-162 <NAK>
A; Residues: 1-162 <NAK>
A; Cross-references: EMBL:X66257; NID:9311892; PIDN:CAA46983.1; PID:9311893
C; Comment: This protein shows a sequence similarity to alpha-amylase/trypain inhibitor
C; Superfamily: wheat alpha-amylase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                     seed allergen RA5 - rice
C,Species: Oryza sativa (rice)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.5%; Pred. No. 11;
Matches 31; Conservative 17; Mismatches 37; Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ROCRGSAAAAEQVRRDCCRQLAAVDDSWCRCEAISHMLGG------IYRELGAPD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: D11430; NID: 9218196; PIDN: BAA01996.1; PID: 9218197 C; Superfamily: wheat alpha-amylase inhibitor C; Keywords: seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GSAFTVWSGPGCNNRAERY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASTKLFFSV--ITVMMLIAMASEMVN------GSAFTVWSGPGCNNRAE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SKCGCSAI-HOKGGYDFSYTGQTAALYNQAGCSG 77
                                      87
30 TVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 66.5; DB 2; Length 157; 22.1%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 VGHPMSEVFRGCRRGDLERAAASLPAFCN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 VAH-----TRFGSSARA-----CN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: JC4887
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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A; Residues: 1-157 <ADA>
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                            A;Gene: nuoF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain F [imported] - Yersinia pestis (stra C;Species: Yersinia pestis (stra C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002 C;Accession: AE0311
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-461 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: SCOEDB: SC1A9.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-251 <SAU>
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                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                        Superfamily: NADH dehydrogenase (ubiquinone) chain F; NADH dehydrogenase (ubiquinone)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                216 VWGKPTCVNNVE--TLCNVPAIIEHGVE--WYQGITAGKSNDAGTK-----LMGFSGRVK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 PAG-PGLAH 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 VNARTDTYWSGDGDVTETLRKLEAYREAGADGVFVPGLTDPARIGSLAARFDVPLNVLYT 193
                                                91 NPFGWKSIF 99
                                                                                                                                    31 VWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARAC 90
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 VNGSAFTVWSGPG----CNNRAERYSKCGCSAIHQKGGYDFSYTGQTAA-----LYN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AEVFPGCRRGDLERAAASLPAFCN 138
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                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                             12.1%; Score 66.5; 34.8%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66.5;
Pred. No. 16;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                 Length 461;
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fa, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica
A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                       nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica C;Species; Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0635
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F;1049-1245/Domain: ATP-binding cassette homology <ABC2>
F;1067-1074/Region: nucleotide-binding motif A (P-loop)
F;1192-1196/Region: nucleotide-binding motif B
F;889,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;432/Binding site: ATP (Lys) #status predicted
RESULT 15
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C;Superfamily: multidrug resistance protein; ATP-binding cassette homology C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; tr: F;1-637,655-1276/Region; duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;409-603/Domain: ATP-binding cassette homology <ABC1>F;426-433/Region: nucleotide-binding motif A (P-loop)F;550-554/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996 C; Comment: This is an integral membrane protein overproduced in multidrug-resistant cel tructurally and functionally unrelated lipophilic antitumor drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kirschner, L.S.

Nucleic Acids Res. 24, 2829-2834, 1996

A;Title: De novo generation of simple sequence during gene amplification.

A;Reference number: S70711; MUID:96313253; PMID:8759018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 19-Jan-2001
C;Accession: A30409; S70711
R;Gros, P.; Raymond, M.; Bell, J.; Housman, D.
Mol. Cell. Biol. 8, 2770-2778, 1988
A;Title: Cloning and characterization of a second member of the mouse mdr gene family.
A;Reference number: A30409; MUID:88302195; PMID:3405218
A;Accession: A30409; MUID:88302195; PMID:3405218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U46839; NID:g1228142; PIDN:AAC52722.1; PID:g1228143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 43-92 < KIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1276 < HSU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;1072/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                             393 FSDVHFSYPSRANIKILKGLNLKVKSGQTVALVGNSGC 430
                                                                                                                                                                                                333 VFFSILIGAFSVGQAAPCIDAFANARGAAYVIFDIIDNNPKIDSFSERGHKPDNIKGNLE 392
                                                                                                                                      60 FS-----YTGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 NPGLWELPF 275
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                       6 LFFSVITVMMLIAMASEMVN-----GSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          20.4%;
                                                                                                                                                                                                                                                                                                                                                          12.0%; Score 66; DB 20.4%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1276;
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Clth, T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;

J.; Stevens, K.

Churcher

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A;Accession: AH0635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>
A;Residues: 1-151 <PAR>
A;Cenetics: references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
C;Genetics: A;Genetics: A;Ge
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Indels	AGCSGVAHTRFGSS/	NDASISOS
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Search completed: January 12, 2003, 09:39:24 Job time : 45 secs

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PGK CHLMU
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VEF GVHA
CSGB SALTY
RA05 MOUSE
CSGB SALTI
OSL3 ARATH
RA14 ORYSA
HXKA YEAST
MDR2 FAT
LMG1 HUMAN
RAG2 ORYSA
YAWI RHISN
MRKC KLEPN
LFC CARRO
LFC TACTR
PRO4 LVAN
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RESULT 2 HXKB_YEAST

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Behlke J., Heidrich K., Naumann M., Mueller E.-C., Otto A., Reuter R., Kriegel T.; Heidrich K., Naumann M., Mueller E.-C., Otto A., Reuter R., "Hexokinase 2 from Saccharomyces cerevisiae: regulation of oligomeric structure by in vivo phosphorylation at serine-14.";
Biochemistry 37:11989-11995 (1998).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-86056943; Pubmed-3905511;
Prochlich K.-U., Entian K.-D., Mecke D.;
"The primary structure of the yeast hexokinase PII gene (HXK2) which is responsible for glucose repression.";
Gene 36:105-111(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 118-126; 175-184 AND 303-313.
STRAIN=ATCC 38531 / Y41;
MEDINE=95255188; PubMed=7737086;
Norbeck J., Blomberg A.;
"Gene linkage of two-dimensional polyacrylamide gel electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolved proteins from isogene families in Saccharomyces cerevisiae by microsequencing of in-gel trypsin generated peptides."; Electrophoresis 16:149-156(1995).
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MEDLINE-97199116; PubMed-9047292;
Heidrich K., Otto A., Behlke J., Rush J., Wenzel K.W., Kriegel T.;
"Autophosphorylation-inactivation site of hexokinase 2 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=W303;
MEDLINE=93311123; PubMed=8322518;
Breitwieser W., Price C., Schuster T.;
Identification of a gene encoding a novel zinc finger protein in Saccharomyces cerevisiae.";
Yeast 9:551-556(1993).
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86120382; PubMed=3003701;
Stachelek C., Stachelek J., Swan J., Botstein D., Konigsberg W.;
"Identification, cloning and sequence determination of the genes
specifying hexokinase A and B from yeast.";
Nucleic Acids Res. 14:945-963(1986).
                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION OF SER-14.
MEDLINE=94114477; PubMed=8286332;
Kriegel T.M., Rush J., Vojtek A.B., Clifton D., Fraenkel D.G.;
"In vivo phosphorylation site of hexokinase 2 in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
MEDLINE=97127827; PubMed=8972578;
Coissec E., Maillier E., Robineau S., Netter P.;
Sequence of a 39,411 bp DNA fragment covering the left end of chromosome VII of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-18, AND PHOSPHORYLATION OF SER-14.
                          JAUG-1987 (Rel. 05, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2000 (Rel. 39, Last annotation update)
HACKNINASE B (EC 2.7.1.1) (HECKNINASE PII)
HAKK2 OR HKB OR HEXI OR YGL253W OR NRB486.
485 AA
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   HXKB YEAST
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                                                                                  -i- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
                                                                                                       Anderson C.M., Stenkamp R.E., Steitz T.A.;
"Sequencing a protein by X-ray crystallography. II. Refinement of yeast hexokinase B co-ordinates and sequence at 2.1-A resolution.";
J. Mol. Biol. 123:15-33(1978)
-!- FUNCTION: MAIN GLUCOSE PHOSPHORYLATING ENZYME. MAY PLAY A REGULATORY ROLE IN BOTH INDUCTION AND REPRESSION OF GENE EXPRESSION BY GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding; 3D-structure; Phosphorylation.

INIT MET

BINDING

110

ATP

BY SIMILARITY).
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GLUCOSE-BINDING (POTENTIAL)
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PHOSPHORYLATION.
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I -> N (IN REF. 2).
G -> V (IN REF. 1).
T -> S (IN REF. 1).
YN -> ST (IN REF. 2).
T -> PH (IN REF. 2).
I -> V (IN REF. 2).
A -> P (IN REF. 2).
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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InterPro; IPR001312; Hexokinase.
InterPro; IPR001312; Hexokinase.
Pfam; PF03727; hexokinase2; 1.
PRINTS; PR00475; HEXOKINASE.
ProDom; PD001109; Hexokinase; 1.
PROSITE; PS00378; HEXOKINASES; 1.
            MEDLINE=78244654; PubMed=355643;
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EMBL; M1181; AAA34697.1; --
EMBL; X94357; CAA64134.1; --
EMBL; Z72775; CAA66973.1; --
EMBL; X67787; CAA96093.1; --
PIR; B13529; KIBYHB.
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STRAIN-MOPN / Nigg:
MEDLINE=20150255; PubMed=10684935;
MEDLINE=20150255; PubMed=10684935;
Mite O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg Bisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumonise AR39.";
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                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
PGK OR TC0065.
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PGY3 OR PC
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Pfam; PF00162; PGK; 1.

PRINTS; PR00477; PHGLYCKINASE.

PROSITE; PS000111; PGLYCERATE KINASE; 1.

Transferase; Kinase; Glycolysis; Complete proteome.

SEQUENCE 403 AA; 43391 MW; 7A80C7A550D89F64 CRC64;
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                                                                                                                                             -!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECI-
DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBSCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANEOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT
CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE002274; AAF73528.1; -. HSSP; P36204; IVPE. TIGR, TC0065; -.
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-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = phospho-D-glyceroyl phosphate.
-!- PATHWAY: Second phase of glycolysis; second step.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                               Endicott J.A., Sarangi F., Ling \dot{\mathbf{v}}.; "Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92135896; PubMed=1685679;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster)
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                                                                                                                                                                                                                                                DNA Seq.
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                                                                                                            SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AALYNOAGC-SGVAHTRFGSSA 87
                                                                                                                                                                                                                                            family.";
deq. 2:89-101(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IALFSEVIQDSATVFWNGPVGVYEVPPFDQGSKAIAQCLASHSSAVTVVGG-----GDA 360
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Pred. No. 2.
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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--- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
--- SIMILARITY: CONTAINS 10.5 LAMININ BGF-LIKE DOWAINS.
--- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                    R HSSP; P13569; INBD.
R INTERPO; IPR003593; AAA_ATPase.
R INTERPO; IPR003439; ABC_transportr.
R INTERPO; IPR001439; ABC_transportr.
R Pfam; PF00005; ABC_transportr.
R Probom; PD000006; ABC_transportr; 2.
R PROSITE; PS00211; ABC_transportr; 2.
R PROSITE; PS00211; ABC_TRANSPORTER; 1.
R ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat; M Multigene family.
F CYTOPLASMIC (POTENTIAL).
T TRANSMEM 58 78 POTENTIAL.
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ATP (POTENTIAL)
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Laminin-like protein C54D1.5 precursor.
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entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                          EMBL; M60042; AAA68885.1; -.
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                         LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 1.
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LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (C-TERMINAL).
LAMININ EGF-LIKE 6 (INCOMPLETE).
LAMININ EGF-LIKE 9.
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Matches 19
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P08183; Q12755; Q14812;

P01-NUC-1988 (Rel. 08, Created)

P01-NUC-1997 (Rel. 35, Last sequence update)

P15-JUN-2002 (Rel. 41, Last annotation update)

Multidrug resistance protein 1 (P-glycoprotein 1) (CD24:

ABCB1 OR PGY1 OR MDR1.

Homo sapiens (Human).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
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MEDILINE-97190336; PubMed-9038218;
Chen G., Duran G.E., Steger K.A.,
Dumontet C., Sikic B.I.;
"Multidrug-resistant human sarcom
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MEDLINE=90094448; PubMed=1967175;
Chen C.-J., Clark D.P., Ueda K.,
                                                                                                             Roninson I.B.;
"Genomic organization of the human and origin of P-glycoproteins.";
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          SEQUENCE OF 1-234 FROM N.A.
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Chen C.-J., Chin J.E., Ueda K., Clark D.P.,
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                                                                                                       Biol. Chem.
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                            rug-resistant human sarcoma cells with a mutant P-glycoprotein,
phenotype, and resistance to cyclosporins.";
. Chem. 272:5974-5982(1997).
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    (CD243 antigen)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japanese population.";
J. Hum. Genet. 47:38-50(2002).
-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21686803; PubMed=11829140;
Saito S., Iida A., Sekine A., Miura Y., Ogawa C., Kawauchi S.,
Higuchi S., Nakamura Y.;
"Three hundred twenty-six genetic variations in genes encoding nine
members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=90290529; PubMed=1972623;
Gekeler V., Weger S., Probst H.;
"mdri/P-glycoprotein gene segments analyzed from various human
leukemic cell lines exhibiting different multidrug resistance
                                                                                                                                                                                                                                                                                                                                                    EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1997) [5]
                                                                                                                                                                                                                                                                                                                                                                                      EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS SER-893 AND THR-893
                                                                                                                                                                                                                                                     M14758; AAAS9575.1; M294247; AAAS9576.1; J W29425; AAAS9576.1; J W29427; AAAS9576.1; J W29428; AAAS9576.1; J W29428; AAAS9576.1; J W29429; AAAS9576.1; J W29431; AAAS9576.1; J W29431; AAAS9576.1; J W29432; AAAS9576.1; J W29433; AAAS9576.1; J W29434; AAAS9576.1; J W29436; AAAS9576.1; J W29436; AAAS9576.1; J W29436; AAAS9576.1; J W29436; AAAS9576.1; J W29440; AAAS9576.1; J W29441; AAAS9576.1; J W29441; AAAS9576.1; J W29441; AAAS9576.1; J W294441; AAAS9576.1; J W294442; AAAS9576.1; J W294442; AAAS9576.1; J W294442; AAAS9576.1; J W294444;  AAAS9576.1; J W294444; J W294444; AAAS9576.1; J W294444; AAAS9576.1; J W294444; AAAS9576.1; J W294444; AAAS9576.1; J W2944444; AAAS9576.1; J W2944444; AAAS9576.1; J W294444; J W294444; J W294444; J W294444; J W294444; J W2944444; J W294444; J W2944444; J W294444; J W294444; J W2944444; J W294444;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS. SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY,
                        A25059;
A34914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/PGY1ID105.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY
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                                                                               AC002457; AAC82531.1; -. M37724; AAA88047.1; -. M37725; AAA88048.1; -. X58723; CAA41558.1; -.
                                                                                                                                                                                                    M29446; AAA59576.1;
AF016535; AAB69423.:
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HGNC:40; ABCB1

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MEDLINE=96068802; PubMed=7595376;
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last nonctation update)
viral enhancing factor (VEF) (Enhancin) (104 kDa glycoprotein)
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                                                                                                                        Pfam; PF00005; AEC tran; 2.
Pfam; PF00664; ABC membrane; 2.
Probom; PD000006; ABC transportr; 2.
SMART; SM00382; AAA; 7.
ATS PROSTTE; PS00211; ABC TRANSPORTER; 2.
ATP-binding; Glycoprofein; Transmembrane; Transport; Repeat; Multigene family; Polymorphism.
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Pred. No. 15;
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A -> S (IN DBSNP:2032582).
/FTId=VAR_013361.
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S -> R (IN REF. 6).

G -> V (IN REF. 1 AND 3).

MISSING (IN REF. 3).

G -> A (IN REF. 3).

Q -> S (IN REF. 3).
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR003439; ABC transportr.
InterPro; IPR001140; ABCtranprtrTM.
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1280 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unipuncta granulovirus enhancin genes.";
J. Gen. Virol. 76:28693-2705(1995).
-!- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPHIC MEMBRANE AND FUSION OF NUCLECCAPELES WITH MIDGUT CELLS (BY SIMILARITY).
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Roelvink P.W., Corsaro B.G., Granados R.R.; "Characterization of the Helicoverpa armigera and Pseudaletia
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit)
CSGB OR AGFB OR STM1143.
Salmonella typhimurium, and
Salmonella enteritidis.
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MEDLINE=98117058; PubMed=9457880;
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MEDLINE-93144699; PubMed=7678765;
Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Nakamura R., Matsuda T.,
"Gene etructure and expression of rice seed allergenic proteins
belonging to the alpha-amylase/trypsin inhibitor family.";
Plant Mol. Biol. 21:239-248(1993).
-I- PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INH:
                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
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MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
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01-JUN-1994
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"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan Leonard S., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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InterPro; IPR003612; AAI.
InterPro; IPR001768; Try/amyl inhbtr.
InterPro; IPR001768; Tryjalpha_amyl; 1.
Pfam; Pr00234; tryp_alpha_amyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA17 ORY
Q01883;
"Nucleotide sequence of a cDNA clone encoding a major allergenic protein in rice seeds. Homology of the deduced amino acid sequent with members of alpha-amylase/trypsin inhibitor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
seed allergenic protein RA17 precursor.
                                                                                                MEDLINE=92289999; PubMed=1376283; Izumi H., Adachi T., Fujii N., Ma Urisu A., Kurosawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                      "Gene structure and expression of rice belonging to the alpha-amylase/trypsin Plant Mol. Biol. 21:239-248(1993).
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Seeq;
MEDLINE=93144699; PubMed=7678765;
MEDLINE=93144699; PubMed=7678765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    Nakamura R., Matsuda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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SIGNAL 1 26 POTENTIAL.
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157 AA; 17118 MW; C8A5495FBFB399E6 CRC64;
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Pred. No. 3
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                                                                                                                  Matsuda T., Nakamura R., Tanaka K.,
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inhibitor family.";
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                                 acid sequence
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
FEBS Lett. 302:213-216(1992).
-!- PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 -QCVGRGASAADEQVWQDCCRQLAAVDDGWCRCGALDHMLSG----IYRELGATEAGHPM 114
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Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BNERGY-DEPENDENT BFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT (ELLS. MOUSE MDR2 IS NOT CAPABLE OF CONFERRING DRUG RESISTANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASTKLFFSVITVMMLIAMASEMVN-------GSAFTVWSGPGCNNRAERY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BELLINES 8302195; PubMed=3405218;
Gros P., Raymond M., Bell J., Housman D.;
"Cloning and characterization of a second member of the mouse mdr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN 28 162 SEED ALLERGENIC PROTEIN RAI7. SEQUENCE 162 AA; 17497 MW; EASCDE021FBA9348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Mulliary resistance protein 2 (P-glycoprotein 2).
ABCB4 OR PGY2 OR PGY-2 OR MDR2.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003612; AAI.
InterPro; IPR001768; Try/amyl inhbtr.
PEAM; PF00234; tryP_albha amyl; 1.
PRINTS; PR00608; AMIASEINHBTR.
SMART; SM00499; AAI; 1.
PROSITE; PS00426; CEREAL TRYP AMYL_INH; 1.
Allergen; Multigene family; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 66.5; DF
21.5%; Pred. No. 3.5;
tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell. Biol. 8:2770-2778(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 -----TRFGSSARA-----CN 91
                                                                                                                                                                                                                                                                                                  EMBL, X66257; CAA46983.1; -. EMBL, D11431; BAA01997.1; -. PIR, S21157; S21157. HSSP; P01085; 1HSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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P21440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- MISCELLANGOUS: IN MOUSE THE MDR GENE FAMILY INCLUDES THREE OR MORE
RELATED BUT DISTINCT CELLULAR GENES.
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 VFFSILIGAFSVGQAAPCIDAFANARGAAYVIFDIIDNNPKIDSFSERGHKPDNIKGNLE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.0%; Score 66; DB 1; Length 1276; 20.4%; Pred. No. 25;
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ATP (BY SIMILARITY).
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MGD; MGI:97569; Abcb4.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transportr; 2.
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Pfam; PF00664; ABC membrane; 2.
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EMBL; M74151; AAA39515.1; -.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSL3 ARATH STANDARD; PRT; 244 AA.
PS0700; Q9T0D2;
PS0700; Q9T0D2;
01-OCT-1996 (Rel. 34, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
0smotin-like protein OSM34 precursor.
OSM34 OR AT4G11650 OR T5C23.80.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:848-852(2001).

-I- FUNCTION: CURLN 15 THE STRUCTURAL SUBUNIT OF THE CURLI. CURL COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FEDERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content is not removed.
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STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                              osmotin-like protein
Gene 191:51-56(1997).
                                                                                                                                                                                                                                                                     Capelli N., Diogon T., Greppin H., Simon P.; "Isolation and characterization of a cDNA clone encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Vilatroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Vilatroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Vilatroel R., De Clercq R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Weller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Clocke R., Berger C., Monffort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenboll M., Bargues M., Terol J., Torres A.,
RA Prishmann D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Prishmann D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnabn M., Murray J., Sheet P., Cordes M., Abb-Threideh J.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
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Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor
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Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mus
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-!- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
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Portetelle D., Perez-Alonso M., Boutry M.,
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MEDLINE=86120382; PubMed=3003701;
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MEDLINE=95400292; PubMed=7670463;
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MEDLINE=86083199; PubMed=3908224;
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Gene 39:95-102(1985).
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STRAIN=S288c / AB972;
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Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Nakamura R., Matsuda T.;
Gene structure and expression of rice seed allergenic proteins
belonging to the alpha-amylase/trypsin inhibitor family.";
Plant Mol. Biol. 21:239-248(1993).
-i. PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
-i. SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR
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Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                           11.9%; Score 65.5; DB 1; Length 244;
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                                                                                                                                                                                                                                                                    44; Indels
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                                                                                                                                               9FBE9A45E9E195E0 CRC64;
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01-JUN-1994 (Rel. 29, Last annotation update)
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PRINTS; PR00808; AMLASEINHBTR.
SMART; SM00499; AAI; 1.
PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
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InterPro; IPR003612; AAI.
InterPro; IPR001768; Try/amyl_inhbtr.
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                                                                                                                                                  26633 MW;
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61 ROCVGTRSPGAVDEQLAQDCCRELAAVDDSWCRCSALNHWVGG------IYRELG 109
MASTKLFFS--VITVMMLIAMASEMVN-------GSAFTVWSGPGCNNRAE 42
                      Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Shibata T., Hanacka F., Murakami Y.; Asasanuma M., Tsuchiya D.P. Seguence including the right telomere of chromosome VI from Saccharomyces cerevisiae.";
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MEDLINE-81049524; Pubmed=7001031;
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"Structure of a complex between yeast hexokinase A and glucose. I.
Structure determination and refinement at 3.5-A resolution.";
                                                                        -----SKCGCSAI-HOKGGYDFSYTGOTAALYNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kopetzki E., Entian K.-D., Mecke D., "Complete nucleotide sequence of the hexokinase PI gene (HXK1) of
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"The adenine nucleotide binding site on yeast hexokinase PII.
Affinity labeling of Lys-"Il by pyridoxal
5'-diphospho-5'-adenosine.";
J. Biol. Chem. 263:7907-7912(1988).
                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-UUN AUG A (EC 2.7.1.1) (Hexokinase PI).
HXKI OR HKA OR YPR053C.
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EMBL; M14410; AAA34698.1; -.
EMBL; X03402; CAA27202.1; -.
EMBL, D50617; BAA09292.1; -.
PIR; A24531; KIBYHA.
PIR; A24531; KIBYHA.
PIR; A28178; A28178.
PDB; 1HKG; 15-0CT-91.
SWISS-2DPAGE; P04806; YEAST.
SWISS-2DPAGE; P04806; YEAST.
SGD; S0001949; HXK1.
InterPro; IPR001312; Hexokinase.
Pfam; PF00349; hexokinase; 1.
Pfam; PF00349; hexokinase; 1.
Pfam; PF003727; hexokinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -|- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
-|- MISCELLANEOUS: IN YEAST THERE ARE THREE GLUCOSE-PHOSPHORYLATING
- ISOENZYMES, DESIGNATED HEXOKINASE I, II AND GLUCOKINASE.
-|- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
-|- DATABASE: NAME=Worthington enzyme manual;
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ProDom; PD001109; Hexokinase; 1.
PROSITE; PS00378; HEXOKINASES; 1.
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  ATP.

GLUCOSB-BINDING (POTENT G)

G -> V (IN REF. 1).

H -> R (IN REF. 1).

V -> K (IN REF. 1).

EN -> VF (IN REF. 1).

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I -> M (IN REF. 2).

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ALIGNMENTS

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8 FSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64 	Query Match 14.1%; Score 77.5; DB 3; Length 486; Best Local Similarity 31.2%; Pred. No. 2; Matches 30; Conservative 8; Mismatches 27; Indels 31; Gaps	Q05538 PRELIMINARY; PRT; 486 AA. Q05538; Q05538; Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 21, Last annotation update) 01-NOV-1996 (TrEMBLrel. 21, Last annotation update) Hexokinase PI (HXK2) HXX2 OR YGL253W. Saccharomyces cerevisiae (Baker's yeast). Enkaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. [1] SEQUENCE FROM N.A. MEDLINE=86083199; PubMed=3908224; KOPETZKI E., Entian K.D., Mecke D.; SEQUENCE FROM IN.A. MEDLINE=86083199; PubMed=3908224; KOPETZKI E., Entian K.D., Mecke D.; SECOTAROMYCES CEREVISIAE."; Gene 39:95-101(1985) ENBL; M141; AAA34699.1; HSSP; P19367; 1QHA. SCD; S000322; HXX2. INterPro; IPR001312; Hexokinase. Pfam; PF00349; hexokinase; 1. Pfam; PF00349; hexokinase; 1. Pfam; PF00377; hexokinase; 1. Pfam; PF00377; hexokinase; 1. PFNOSITE; PR00475; HEXOKINASE. ProDom; PD001109; Hexokinase; 1. PROSITE; PR00378; HEXOKINASES; 1. PROSITE; PS00378; HEXOKINASES; 1.	IUT 1

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J. Cell Sci. 111:1545-1554(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
VCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tosato V., Ciarloni L., Bianchettin G., Bruschi C.V., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydra magnipapillata (Hydra).
Eukaryota, Metazoa, Chidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
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Best Local Similarity 24.6%; Pred. No. 11;
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MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR001865; Ribosomal S2.
PROSITE; PS00962; RIBOSOMAL S2_1; UNKNOWN_1.
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SEQUENCE 1558 AA;
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"The division and cell wall gene cluster of Enterococcus hirae S185.";

"The division and cell wall gene cluster of Enterococcus hirae S185.";

DNA Seq. 9:149-744232.1;

Interpro; IPR004225; PBP Cterm.

Interpro; IPR004225; PBP Cterm.

Interpro; IPR00451; PBP Gimer.

Interpro; IPR00460; Transpeptdase.

Pfam; PF03704; PBP C; 1.

Pfam; PF03705; Transpeptiase; 1.

SEQUENCE 730 AA; 80947 MW; C928FFICI0E810BB CRC64;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes, Bacillus/Clostridium group; Lactobacillales;
Enterococcaceae; Enterococcus.
NCBI_TaxID=1354;
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                                                                         Match 13.6%; Score 75; DB 5; Length 254; Local Similarity 27.3%; Pred. No. 1.9; es 24; Conservative 14; Mismatches 24; Indels
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EMBL; AF043907; AAC39121.1; -. SEQUENCE 254 AA; 25393 MW; 649BAB00B3BEABF9 CRC64;
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Last annotation update)
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MEDLINE=99319897; PubMed=10392726;
Stephensen C.B., Casebolt D.B., Gangopadhyay N.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
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RESULT 6
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Virus Res. 60:181-189(1999).
EMBL; AF124987; AAD32991.1; -.
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
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Virus Res. 60:181-189(1999).
EMBL; AF124986; AAD32990.1; -.
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                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Alcohol dehydrogenase (Acceptor) (EC 1.1.99.-).
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                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                       124 MIRMASAMILGSKHV-----GCCTHSDRFYRLSNELAQVLTEVVHCTGGFYFKPGGTTSG 178
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                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCG-----CSAIHQKGGYDFSYTGQTAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DGTTAYANSAFNI FQAVSANVNKLLGVDSNACNNVTVKSI
                                                                                                                                                                                                                                                                                                ----DGTTAYANSAFNIFQAVSANVNKLLGVDSNACNNVTVKSI 218
                                                                                                                                                                                                                                                                                                                                                  LYNQAGCSGVAHTRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307
307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 70; I ilarity 25.0%; Pred. No. 8. Conservative 13; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34500 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2A3AD4C643AC86E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2A3AD4C643AC9711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                     -GSSARACNPFGWKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                  532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                        98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

EMBL; AE009671; AAL53581.1; -

InterPro; IPR00172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.

PROSITE; PS00624; GMC_OXRED_2; 1.

Oxidoreductase; Complete proteome.

SEQUENCE 532 AA; 58225 MW; F15B57645D149ADD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   057484
057484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=29459;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=93015947; PubMed=1400373;
                                                                                                                                                                                                                                                                             "Primary structure and expression of a chicken laminin beta chain: evidence for four beta chains in birds.";
Matrix Biol. 16:471-481(1998).
                     InterPro; IPR001886; LamNT;
pfam; pF00053; laminin EGF; 13.
pfam; pF00055; laminin Nterm; 1.
pRINTS; PR00011; EGFLAMININ.
SMART; SM00180; EGF_Lam; 13.
                                                                                                                                              HSSP; P02468; iKLO.
InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Rear J.J.;
                                                                                                                                                                                                                                                       EMBL; AF038555; AAB92586.1;
                                                                                                                                                                                                                                                                                                                                                              Liu
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98209634; PubMed=9550264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 12.6%;
Local Similarity 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAHTRFGSSARACNPFGWKSI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WGWDDV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTTEAEPGLNGRSLNYPRGKVLGGCSSINGMIYMRGQACDYD-----LWRQAGCDG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTVWSGPGCNNRAERYSK----CGCSAIH-----QKGGYDFSYTGQTAALYNQAGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
  SM00180;
                                                                                                                                                                                                                                                                                                                                                              Swasdison S., Xie W., Brewton R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laminin B1 chain variant in Chem. 267:20555-20557(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  LamNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69.5;
Pred. No. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                   Mayne
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                                                                                                                                                                                                                                                                                                                                                                      70
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ب
                                                                                                                                                                                                                                                                                                                                                                                                                                      300 ATADGMVHGRCVCKHHTQGLNCERCEDFYHELPWRPAEGSSTWACRRCDCNEHSRRCHFD 359
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    18 AMASEMVNGSAFTVWSGPGCN-NRAERY-----SKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
PROSITE; PS00339; AA TRNA LIGASE II 2; UNKNOWN 1.
PROSITE; PS01022; EGF 1; ÜNKNOWN 10.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01248; LAMINN TYPE EGF; 12.
EGF-like domain; Glycoprotein; Laminin EGF-like domain; Repeat.
SEQUENCE 1792 AA; 195723 MW; 4A4CBE0206F6A600 CRC64;
                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                               Query Match 12.6%; Score 69.5; DB 13; Length 1792; Best Local Similarity 25.0%; Pred. No. 61; Matches 25; Conservative 9; Mismatches 41; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N 11)
N 11)
N 11)
N 11)
N 12)
N 12)
N 12)
N 12,
Nakaichi M.;
Uozumi K., Nakaichi M.;
Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases.
I submitted (Jul-2001) to the EMBL/GenBank/DDBJ databases.
N EMBL; AB06629; BAB83959.1;
N InterPro; IPR001399; AAA ATPase.
N InterPro; IPR001399; AAA ATPase.
DR Fam; PF00664; ABC membrane; 2.
DR Pfam; PF000006; ABC transportr.
DR ProDom; PD000006; ABC transportr; 1.
DR SMART; SM00382; AAAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 69; DB 6; Length 668; 25.5%; Pred. No. 24; tive 12; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    668 AA; 73546 MW; F8CD80F7C934B31A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Multidrug resistance p-glycoprotein (Fragment).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Multidrug resistance p-glycoprotein.
MDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 MAVFLATGNTSG----AVCDGCQHNTMGRHCHLCKPFYYK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ---FSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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Local Sir.
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SEQUENCE
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046605
AD 046605
DT 01-JUN
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          SO KE BER
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Schwarz-Romond T., Asbrand C., Bakkers J., Kuhl M., Schaeffer H.-J., Huelsken J., Behrens J., Hammerschmidt M., Birchmeier W.; "The Ankyrin Repeat Protein Diversin Acts in the Wnt Signaling Pathway and Controls Embryonic Axis Formation."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY026320; AAXIS806.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||||: | | | : |-|| : 335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
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Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                               EMBL, APC45016, AACC2113.1, -...

InterPro; IPR001599; AAA ATPase.
InterPro; IPR001399; ABC Transportr.

R InterPro; IPR001399; ABC Transportr.

R Pfam; PF000664; ABC membrane; 2.

R ProDom; PD000005, ABC Transportr; 2.

R SWART; SM00382; AAA; 2.

R PROSITE; PS00211; ABC TRANSPORTER; 2.

R PROSITE; PS00211; ABC, TRANSPORTER; 2.

R PROSITE; PS00211; ABC, TRANSPORTER; 2.

R ATP-binding; Transport.

SEQUENCE 1280 AA; 141524 MW; 762DD5AFF4C73306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         12.5%; Score 69; DB 6; Length 1280; 25.5%; Pred. No. 48; tive 12; Mismatches 33; Indels ;
                                                                                                                              Puel O., Lepage J.F., Alvinerie M., Galtier P., Pineau T., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 68; DB 11; Length 712; 23.5%; Pred. No. 34; tive 21; Mismatches 37; Indele ::
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PROSITE; PS50297; ANK REP REGION; 1.
SEQUENCE 712 AA; 77934 MW; BC0344DA544E731A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 ----FSY-----TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann
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Pfam; PF00023; ank; 8.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 8.
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Matches 25, Conservative
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                                                                                             SEQUENCE FROM N.A.
                                                         NCBI_TaxID=9615;
                                                                                                                  TISSUE=COLON;
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Best Local (
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Q9WQ75;
01-NOV-1999
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Therry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                 Viruses; ssRNA
                                                                                                                              01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                 138 -----GYSGYG-----GGYPGMYGGGMGGSYGSSSWGSYSSSRSG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geisel C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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Q09943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                ransmissible gastroenteritis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                         37 CNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHSTTLFFVVFGILVAVSLAFDDLNHPKNLQWRSSEGSRVKRWGGWGGGYPGGYGGGYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U28731; AAA68294.1; -.
NCE 184 AA; 20062 MW; EF19A9A6C96B175A CRC64;
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                                                                                        (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence
(TrEMBLrel. 19, Last annotated RNA polymerase (Fragment).
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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        positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans cosmid F12A10.";
) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 34; Indels
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                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67.5;
Pred. No. 9.
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DNA stage; Nidovirales;
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RESULT 14
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                                                                                                                          IJkel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Goldbach R.W., Vlak J.M.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF169823; AAF33660.1; -
                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         IJkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D. Goldbach R.W., Vlak J.M., "Sequence and organization of the spodoptera exigua multicapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93286555; PubMed=8509757;
Zuidema D., van Oers M.M., van Strien E.A., Caballero P.C., Klok E.J.,
Goldbach R.W., Vlak J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20036646; PubMed=10567663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spodoptera exigua nuclear polyhedrosis virus.", J. Gen. Virol. 74:1017-1024(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and transcriptional analysis of the p10 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 596-653 FROM N.A.
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Viruses; dsDNA viruses, no RNA stage; I
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EMBL; AF124992; AAD32996.1; -
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Stephensen C.B., Casebolt D.B., Gangopadhyay N.N.;
"Phylogenetic analysis of a highly conserved regio
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                                     Similarity
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307 AA;
             Conservative
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                                                                                                     74213 MW; DADAD68F070FE0BC CRC64;
12.2%; Score 67; DB 12; Length 653; 33.3%; Pred. No. 40; tive 9; Mismatches 15; Indels
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RN 113
RP SEQUENCE FROM N.A.
RX MEDLINE=98055454; PubMed=9195076;
RX Doliana R., Bellina I., Bucciotti F., Mongiat M., Perris R.,
Doliana R., Bellina I., Bucciotti F., Mongiat M., Perris R.,
Colombatti A.;
Colombatti A.;
The human alpha3b is a 'full-sized' laminin chain variant with a more RT widespread tissue expression than the truncated alpha3a.";
RY MEDLINE-STO(1997).

BEREL 147:65-70(1997).

BEREL AF005268; AACS1867.1;
BEREL PERO IPRO00649; Leminin EGF.

BEREL PROONS3; Inaminin Nerm:
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BEREN PROSITE; PSO0022; EGF I; UNKNOWN 10.
BEREN PROSITE; PSO0022; EGF I; UNKNOWN 10.
BEREN PROSITE; PSO0022; EGF I; UNKNOWN 10.
BEREN PROSITE; PSO10228; LAMININ TYPE EGF;
BEREN PROSITE; PSO10229; EGF I; UNKNOWN 10.
BEREN PROSITE; PSO10229; EGF I; UNKNOWN 10.
BEREN PROSITE; PSO10229; EGF IINE GOMAIN; Repeat.
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12.2%; Score 67; DB 4; Length 1486;
Best Local Similarity 28.1%; Pred. No. 95;
Matches 27; Conservative 8; Mismatches 23; Indels 38; Gaps
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                                         Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
43 RYSKCGCSAI-----HQKGGYD-----FSYTGQTAALYNQAGC---SGVAHTRFGS 85
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1486 AA; 162496 MW; F2ESEB7EB522E98C CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 45	4	43	42	41	40	u	c 38	w	36	ú	C 34	υ u	32	c 31	30	29	c 28	27	26	c 25		23		c 21	20		c 18			15	C 14	13	12	1	10	ه م	. מ		י ע י נ		4	ω	22	щ	Result
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ALIGNMENTS

REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 MIRNAAP1 LOCUS DEFINITION
Macadamia, Froceaceae; 1 (bases 1 to 493) Marcus, J.P., Goulter, K.C., Green, J.L., Harrison, S.J. and Manners, J.M.	Macadamia integrifolia. Macadamia integrifolia Macadamia integrifolia Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatrophyta: Maranliophyta; Ordinory, Depreyora, Tracheophyta;	Y10903	MIRNAAPI 493 bp mRNA linear PLN 05-JUN-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Purification, characterisation and cDNA cloning of an antimicrobial
                                                                                                                                      Submitted (30-JAN-1997) J.P. Marcus, Cooperative Research Centre for Trop., Plant pathology,, 5th Level John Hines Building,, The University of Queensland, Brisbane, QLD 4072, AUSTRALIA Location/Qualifiers
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                                                                                                                                                                                                                                     organism="Macadamia integrifolia"
                                                                                                                                                                                                                                                                                                                                                                /gene="AMP1"
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100.0%; Pred. No. 3.2e-121
:ive 0; Mismatches 0;
                    peptide from Macadamia integrifolia
Eur. J. Biochem. 244 (3), 743-749 (1997)
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/clone="pGM7*2"
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/gene="AMP1"
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Direct Submission

Submitted (21-MAR-2001) Sanger Centre, Hinkton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequesteGeanger.ac.uk

On Nov 20, 2000 this sequence version replaced gi:11137809.

During sequence assembly data is compared from overlapping clones,
Where differences are found these are annotated as variations
together with a note of the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbrevations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw.; SWISSPROT, Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
IMPORTANT: This sequence is not the entire insert of clone
RP11-20312 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP1-328K6 is at 100321 in this sequence.
The true left end of clone RP1-328K6 is at 100 in this sequence.
The true left end of clone RP1-328K6 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality as
compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 succlone; and the
new plasmid subclone or more than one M13 succlone; and the
secupressions and repeats; all regions yere covered by the Jone, here it branty RPC1-11.1 constructed by the group of Pieter de Jong.
For Eutrher details see
                                                                                                                                                                                                             AL359378 100919 bp DNA linear PRI 09-APR-2001 Human DNA sequence from clone RP11-203H2 on chromosome 6 Contains an STS and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="L2 repeat: matches 2564. .2672 of consensus"
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/clone lib="RPCI-11.1"
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Direct Submission
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/note="match: GSS: Em:AQ779724"

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/note="match: GSS: Em:B82645"
4413. .4740
                                                                                                                                                                                                                                             32387. .33129
/note="AluJo repeat: matches 1. .296 of consensus" 3333. .33573. .33573 // start and the start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start and start a
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| note="30 copies 2 mer at 83% conserved
| 0704. .10741
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/note="21_copies 2 mer cc 78% conserved"
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3184. .8463
note="AluSx repeat: matches 6.
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/note="LTR32 repeat: matches 15. .471 of consensus"
7809. .7895
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                                                                                                                                                                                       note="LTR1 repeat: matches 2. .785 of consensus"
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,2550. .12595
note="L1MC3 repeat: matches 7693. .7737 of consens
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| note="15 copies 2 mer ac 100% conserved"
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                                                                                                                                                                                                                                                                                                                      note="MLT1A1 repeat: matches 10. .365 of consensus" 1883. .32342
                                                                                                                                                                                                                                                                                                                                                                                                note="L1MD2 repeat: matches 5830. .6070 of consensus' 0131. .30479
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9311. .28547
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1257. .21564
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)3. .27220
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9. .21256
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2. .26553
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3. .22367
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.22057
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                                                                                                                                                                                                                                                                         .490 of consensus"
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361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCTTCTATGTTTTTCAAGTGT 420
                                                                                        /note="match: GSS: Em:AQ414205" complement(54955. .55495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51187. .51345
/note="LIPA16 repeat: matches 5913.
complement (51373. .51986)
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/note="LIPA10 repeat: matches 5719. .6158 of consensus"
complement(41095. .41838)
/note="match: GSS: Em:AQ374227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (41129. .41828)
/note="match: GSS: Em:AQ374468"
                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ717563"
53193. .53499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (48046)
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36453; .36763
                                                                                                                                                                                                                                                      note="match:
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complement (48046. .48587)
roote="match: GSS: Em:AQ589537"
i8086. .48137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluY repeat: matches 1. .310 of consensus"
|3832. .44317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1PA8 repeat: matches 5822. .6162
7366. .37399
note="17 copies 2 mer gt 88% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 150.
1634. .51930
note="AluSx repeat: matches 1.
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8974. .49516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER3 repeat: matches 1. .209 of consensus" 6372. .46675
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                                                                                                                                                                                                                                                                        3575. .53969
                                                                                                                                                                                                                                                                                                                                                note="match:
3173. .53610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: GSS: Em:AQ394900"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 1474. .2083 of 0479. .50545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3130. .38308
note="MER5A repeat: matches 2. .189 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LIMB5 repeat: matches 5576. .6152 of consensus"
3857. .46065
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                                                                                                                                              50.5%;
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                                                                                                                                            Score 41.2; DI
Pred. No. 1.7;
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                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 Em: AQ044785"
                                                                                                                                                             DB 9; Length 100919;
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Drive, Malnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:14579767.

Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Frinishing Completed at Stanford Human Genome Center
Www.sigc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 168575)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 161903 TGTGAGTCTTCCAGCATTGTTTTTTTCTCTTTCAAAACTGTTTTGGCTATTCTCTTTCATA 161962
                                                       42127 ATCTATGTCTGTGTATGTATTTATAGACTATATAATCTATATTGTATATTATTATGTAT 42186
                                      421 ATAATTAGAGAGATGCATGGATATATAAATAAGTAAAAGCTAGGGTATCACCATGTG 480
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Homo sapiens chromosome 5 clone RP11-76H13, complete sequence
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/db_xref="taxon:9606"
/chromosome="5"
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DOE Joint Genome Institute.
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AC091989.3 GI:15375178
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Matches 76; Conservative
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SHGC-81786 G53001
SHGC-84076 G53749
                                                                                                                                    42247 ATTTTGTCCACC 42258
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Direct Submission
Submitted (15-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.
Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
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      HTG 15-APR-2002
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1 (bases 1 to 110913)
Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Weissenbach, J. and Quetier, F., Scarpelli, C., Salanoubat, M., Oryza, Strive and Cherier, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 86237 CTAACCTAGCTAATACTCTACAATATCTGGTCAAACCCAATTGCGCTCCAAATTCCTAAT 86296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 TIGGGICCAGIGCCAGGGCAIGCAACCCITTIGGITGGAAGAGTAICTICAICCAAIGCT 376
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                              Oryza sativa chromosome 12 clone Monsanto-OJ1494_F10, SEQUENCING IN PROGRESS ***, in ordered pieces.
linear
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10497 bp contig from 1 to 10497
2346 bp contig from 10598 to 12943
3998 bp contig from 10142 to 13117
15976 bp contig from 17142 to 13117
24871 bp contig from 13118 to 58088
1124 bp contig from 58189 to 59319
19907 bp contig from 58189 to 59319
4909 bp contig from 59413 to 79319
4909 bp contig from 84429 to 110913.

* NOTE: This is a "working draft' sequence.
This sequence will be replaced
   DNA
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/clone_lib="Monsanto"
22828 c 22735 g 32434 t
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                                                                                                              AL713902.1 G1:19701072
HTGS PHASE2; HTGS_ACTIVEFIN.
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Oryza sativa
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/sub_species="japonica"
/db_xref="taxon:4530"
   110913 bp
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2 (bases 1 to 110913)
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hes 95; Conservative
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Db 119093 ATGGGTGT 119086

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437
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ATGGATAT 444
                                     AAAATACATGACTAACTGAACCGTAAATTATAATAGTACTGTAGTGAATTAAAGATATCT 119094
                                                                         ATGGATAT 444
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Submitted (26-JUL-2002) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Heb : www.genoscope.cns.fr)

IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence.

Work on the sequence is in progress and the release of this data is
based on the understanding that the sequence may change as work
continue. The sequence may be contaminated with foreign sequence
from E.coli, yeast, vector, phage, etc.

NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced
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1 (bases 1 to 137936)

Choisne,N., Orjeda,G., Cattolico,L., Demange,N., Wincker,P., Segurens,B., Pelletier,E., Scarpelli,C., Salanoubat,M., Weissenbach,J. and Quetier,P.

Oryza sativa chromosome 12 sequencing
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Oryza sativa chromosome 12 clone OSJNBa0041K23,
PROGRESS ***, in ordered pieces.
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN
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/sub_species="japonica"
/db_xref="taxon:4530"
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29563 c 29308 g 40105 t
                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="OSJNBa0041K23"
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                                                                                                                                                                                                                                                                                            Score 39.2; DB 2; Pred. No. 5.6; 0; Mismatches 93;
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SEQUENCING IN
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AUTHORS
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ORGANISM
                                                                                        Db 126114 CTAACCTAGCTAATACTCTACAATATCTGGTCAAACCCAATTGCGCTCCAAATTCCTAAT 126055
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ORIGIN
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                                                                                                                                                                                                                                                                                                       Best Local Similarity
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       125994
                                                                                                                                                                                                                     257 CTGGACAAACTGCTGCTCTACAACCAGGCTGGATGCAGTGGTGGTGTTGCACACCACGAGGT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                           377 AGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAGAGATGC 436
AAAATACATGACTAACTGAACCGTAAATTATAATAGTACTGTAGTGAATTAAAGATATCT 125935
                                                                                                                                      TTGGGTCCAGTGCCAGGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCT 376
                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1062 bp contig from 1 to 1062
933 bp contig from 2063 to 2995
583 bp contig from 3996 to 4578
2449 bp contig from 5579 to 8027
66895 bp contig from 9028 to 75922
67856 bp contig from 76923 to 144778.
* NOTE: This is a 'working draft' seguence.
* NOTE: This is a 'working draft' seguence.

* This record will be updated with the finished sequence

* La soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Work on the sequence is in progress and the release of this data based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E_coli, yeast, vector, phage, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-FEB-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salse, J., Choisne, N., Orjeda, G., Regad, F., Lorieux, M., Delseny, M., Robert, C., Brottier, P., Wincker, P., Cruaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contigs composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa chromosome 12 sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artiguenave, F., Saurin, W., Salanoubat, M., Quetier, F. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /clone="0SJNBa0041K23"
/clone_lib="CUGI Nipponbare BAC"
30027 c 29723 g 39633 t 5033 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryza sativa"/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                    50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .144778
                                                                                                                                                                                                                                                                                                    Score 39.2;
Pred. No. 5.
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6
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SEQUENCING IN
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BASE COUNT
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AC090757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (189-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Tel:81-42-778-9923, Pax:81-42-778-9924) on May 30, 2000 this sequence version replaced gi:7678794.

Center: RIKEN Genome Center Center (GSC)
Center code: RIKEN Genomic Sciences Center (GSC)
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                                                                                                                                                                                          HTG 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 152137)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 152,137 genomic DNA of 18922
Published Only in DataBase (2000)

2 (bases 1 to 152137)
                                                                                                                                              152137 bp DNA linear HTG 30-MAY.
Homo sapiens chromosome 18 clone RP11-701G2 map 18q22, WORKING
AP001932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
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134717 73705 contig of 138989 bp in length
103320 103329 contig of 28414 bp in length
103320 144710 contig of 26510 bp in length
129930 144710 contig of 14781 bp in length
144811 152137 contig of 7327 bp in length
5 sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-701G2.
                                                    Db 125934 ArddGrigr 125927
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437 ATGGATAT 444
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                                                                                                                                                                                                                                                                                                              VERSION
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campoplano, A., Choepel, Y., Collargelo, M., Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lones, C., Karatag, A., Liu, G., MacLean, C., Macdonald, P., Liu, G., MacLean, C., Macdonald, P.,
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Homo sapiens chromosome 18 clone RP11-701G2 map 18, WORKING DRAFT
SEQUENCE, 1 ordered piece.
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1 (bases 1 to 153485)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-70162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .34616
/note="assembly_fragment clone_end:T7 vector_side:right"
34717. .73705
/note="assembly_fragment"
73806. .103219
/note="assembly_fragment clone_end:SP6 vector_side:left"
103320. .129829
/note="assembly_fragment"
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                                         34617 34716: gap of 100 bp
34717 73705: contig of 38989 bp in length
73706 73805: gap of 100 bp
73806 103219: contig of 29414 bp in length
103220 103319: gap of 100 bp
103320 129829: contig of 26510 bp in length
                                                                                                                                                                                                                    129830 129929: gap of 100 bp | 129930 144710: contig of 14781 bp in length
                       34616: contig of 34616 bp in length
                                                                                                                                                                                                                                                                          144711 144810: gap of 100 bp 144811 152137: contig of 7327 bp in length. Location/Qualifiers
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ture 144811. .152137
/note="assembly_fragment"
49625 a 26249 c 26522 g 49241 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="RP11-701G2"
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Best Local Similarity 63.2%;
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    be preserved.

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Db 103951 TATATATACATATATATATATATATATATA 103985
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                                                                                                                                                                                   360 TATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bource
                                                                                                                                                                                                                                                                                                       Local
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                                            TATAATTAGAGAGATGCATGGATATAATAAATA 454
                                                                                                                      60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly_fragment
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

153485: contig of 153485 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                     50428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 155000; agarose-fp
Insert size: 153485; sum-of-contigs
Quality coverage: 9.5 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 153438 bases at least Q30 Consensus quality: 153480 bases at least Q30 Consensus quality: 153480 bases at least Q30 Consensus quality: 153480 bases at least Q30 Consensus quality: 153480 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: L12250 Center clone name: 701_G_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ Genome Center Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-701G2"
/clone_lib="RPCI-11 Human Male BAC"
26340 c 26956 g 49761 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                             7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                          26956 g 49761 t
                                                                                                                                                                                                                                                                                         Score 39; DB;
Pred. No. 6.3;
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                     DB 2; Length 153485;
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COMMENT
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AUTHORS
TITLE
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AC019240
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE 3 (bases to 17502)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bouslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Bouslavkiy, L., Boukhgalter, B., Arderson, S., Barna, N., Canppiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McChaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Maylor, J., Nguyen, C., Norbu, C., Norman, C., H., Murphy, T., Maylor, J., Nguyen, C., Norbu, C., Norman, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                          Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 28, 2001 this sequence version replaced gi:14190661. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Contact: sequence_submissions@genome.wi.mit.edu------ Project Information
                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                     -- Genome Center
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clone_lib="RPCI-11 Human Male BAC"
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complement(18230. .18722)
/rpt family="LiME1"
complement(18730. .18722)
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complement(18730. .19362)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement 16106. .16413)
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complement (16479. .17248)
/rpt family="LiME1"
complement (17249. .17791)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13134 ..13164

"Type family="AT rich"

complement (14050. .14153)

/rpt_family="MIR"

1272. .12538

/rpt_family=" (TCTA) n"

15321. .11492
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complement (2585. .3711)
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complement (4269. .4381)
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/organism="Homo ·sapiens"
/db_xref="taxon:9606"
/chromosome="18"
Center project name: L1037
Center clone name: 510_D_19
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/rpt_family="AT_rich"
6211. .6664
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="(TAAA)n"
5684. .15842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="AT_rich"
1393. .11567
                                                                                                                                                                  1456. _1482
/rpt_family="AT_rich"
1673. .1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="L1MC4a"
3134. .13164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="LTR37B"
5525. .1545?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15684. 15842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="AluSx"
5654. .15683
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3607 .8270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260. .9551
rpt family="AluSg"
1215. .11237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    014. .7177
rpt_family="LIMDb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="L1MD2"
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="L1MDb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L2"
9169. .9257
/rpt_family="L2"
9260. .9551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="MLT;
complement(17792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .15683
                                                                                                                         /map="18
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                                                                                             Submitted (13-JUL-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18141352.

Center: Baylor College of Medicine
Center code: BCM
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                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Project Information
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22, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                            Department
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 54814 bases at least Q40
Consensus quality: 59343 bases at least Q30
Consensus quality: 63485 bases at least Q20
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AC113238 149767 bp DNA linear HTG 27-FEB-2002
Felis catus clone RP86-252E8, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

1 (bases 1 to 149767)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffack, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Helo, S.L., Idol, Ju.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B., Matrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Wiggins, L., Young, A., Zhang, L.H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-FEB-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: 252E08

Center clone name: 252E08

Center clone name: 252E08

Sequencing vector: plasmid, n/a; 100% of reads
Sequencing vector: plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 147596 bases at least Q40
Consenus quality: 147747 bases at least Q20
Insert size: 135000; agarose-fp
Insert size: 149367; sum-of-contigs
Quality coverage: 10.56x in Q20 bases; sum-of-contigs
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9219 9218: gap of unknown length
9219 17046: contig of 7828 bp in length
7047 17146: gap of unknown length
1900 34999: gap of unknown length
1900 57007: contig of 17753 bp in length
1008 57107: gap of unknown length
1008 57107: gap of unknown length
1008 149767: contig of 92660 bp in length.
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/clone="RP86-252E8"
/clone_lib="RP86"
                                                                                         AC113238
AC113238.1 GI:18958665
HTG; HTGS_PHASE1; HTGS_DRAFT.
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2 (bases 1 to 149767)
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gap of unknown length
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gap of unknown length
contig of 3714 bp in length
gap of unknown length
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94967: gap of unknown length
99862: contig of 4895 bp in length.
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unknown length
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87785: contig of 4404 bp in length
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/clone="CH230-134K22"
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                                                         contig of 1984 b
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gap of unknown
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                                                                                                                                                                                   Submitted (29-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GenetD may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                        Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,B., Quail,M.A., Platzer,M., Rosenthal,A. and Noegel,A.A.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG: HTGS PHASE2.
Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum chromosome 2 map 1058125-1163590 strain
                                                                                                                                                         Agency
                                                                                                                                                                            Funding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 105470)
Gloeckner, G., Eichinge
                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                                                                                                                                                                                                                                                                                                                                       Baumgart
                                                                                                                   gency : Deutsche Forschungsgemeinschaft (DFG)
NOTE: This is a 'working draft' sequence.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40836
                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 105470)
                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium Genome Sequencing Consortium
                                                                                the finished sequence as soon as it is available and accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                     Location/Qualifiers
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32347 c 32343 q
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53.7%;
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                                    discoideum"
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CHNDLIPRIMMIYNKEKGQVKFIDFEYSGYNFRGYDIGNFFCEFSGLDLDYTKYPSIEI
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SNSQLLLSSSSDSAIKESTTISTSTSTSTSTSTSPSLENSTLSPRNMNTQTSS
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PEWTHVSEHAKAFIRNLIVKDPDQRHTAKQCLDDLWLSGSDQSIGSAADLHSHFAEKM
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                                                                      join(22173. .22264,2237)
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complement(join(5120. .5211,5342. .6798,6919. .733)
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I VGSS I KLDRDI EFLETI FI DLTTRLI LEKE I DPKI NNNNNNNNNNNNNNNNNNNNNN
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DEEYFADFCLCNPPFFFKDLNENNNKNNNPKSNCTGSVNEMYTDGGEFFFYKRIIKES
                                                                                                                                                                                                EISLGHEPNLLRFSIGMLMLIAAMFLSSILGIJQEHTYKLYGKDRHYETIFYSNNDIL
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SIRKFLSIIISVIYFNNHFTSLLFTGTILVFLGTFMYSTSGKVIEKPLPPTKQVKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNLUFRQELVGMNVSYYFANEKMDSKCSNAKTNVYAEPLHVCDEDNQIKVSYNYLTYQ
DAINDLMDROSCNEVI FINGCEENVIITSILKGYTCSPIKVNDFEAWTYSTCDENSMLSY
ICSEPTCFIGNCYAI PNVYKNSTQCVPGRDLDGNIADGIYYKFVPKLKSQPKDSSPTP
SQTSTPISEDEDPNHSSKVFASIALIIFGLLLSSL"
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TQTSTLWQTVSLPPILPNEQYYLEYFLSSQFETNINPVLNVYVDNRPVASYNGNLLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKILLTFILLINLIIVKSDLVVKTNVYNSPGCTGGVNKTVLHSH
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note="ORF ID:dd_00653"
codon_start=1
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/protein_id="AAL99330.1"
/db_xref="G1:19807761"
                                                                                                                                                                                                                                                                                                                                                                                                                 complement (23858. .24619)
/note="ORF_ID:dd_00658"
/codon_start=1
xref="GI:19807760"
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Submitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, Cubmitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk

On Mar 11, 2001 this sequence version replaced gi:12961937.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                  GRSKRNKTEQYLKEWVASNGNQKRERLEDSIPDLPENREAREFLRNAPTKGLHQPLGK
EVVNQCWKCKFYGHAALECTQTNP FASTKLKKREDEMIQYNDHDDFGORNNKNNIN
INNINNINNIN THKDR INKINTNDENIDNINKANKRQKKLKQLQELLARAERIERKRK
EKKRKKKKIKKKITKASKKSHHRHSSDSDSGGGSSDSDSDLSKDESYSSNESE"
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Human DNA sequence from clone RPI1-326D19 on chromosome 13,
                                                                     /trānslation="MDRRDYSKEKYKYGDNDKDRRFSNDKIRHNFDEFTMPSNDRRDR
DKDIDRYRDRYRDRYRDRDRDRDRDRDRDRBRERERERERERSRSPNRNYSRNNNSSS
                                                                                                                               YNSNNSSSSFDDGYKYRDMDRERDKYRENKRFDSSRNNEDHRSSIRPLSYDGYDDDY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the feature table with their source databases: Em:, EMBL, Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
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/note="ORF_ID:dd_01572"
/codon_start=1
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/protein_id="AAL99333.1"
/db_xref="GI:19807764"
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/note="ORF_ID:dd_01574"

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11-326D19 is from the library RPCI-11.2 constructed by the Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is the entire insert of clone RP11-326D19 The t end of clone RP11-229I7 is at 61034 in this sequence. Location/Qualifiers
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/db_xref="taxon:9606"
                                                                        23694. .23996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluJo repeat: matches 93. .282 of consensus"
16400. .16453
| Marke="27 copies 2 mer ta 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="1
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1330. .7197
note="17 copies 4 mer atag 88% conserved"
136. .7195
                                                                                                                                                                                                                                                                                                                                                              note="18 copies 2 mer tt 86% conserved"
10660. .21162
note="11MBB repeat: matches 5649. .6161 of consensus"
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                              note="L1M4 repeat: matches 3074. .3310 of consensus"
94000. .24037
                                                                                                                                                                                    note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                         note="21 copies 4 mer gaag 77% conserved"
                                                                                                                                                                                                                                                                                                 note="L1 repeat: matches 4045. .4250 of consensus" 2022. .22105
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                                                                                           note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                               note="L1M4 repeat: matches 3360. .4073 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSp repeat:
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                                                                                                                note="L1M4 repeat: matches 3310. .3360 of consensus"
3303. .23693
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7. .10246
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/note="THE1C r/
36028. .36144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28572. .28675
/note="L2 repeat: matches 210. .314 of consensus"
29376. .3119
/note="L1 repeat: matches 3165. .4993 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26649. .26903
/note="AluSg repeat: matches 1. .255 of consensus"
27125. .27152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1PA3 repeat: matches 5378. .6146 of consensus"
25498. .26057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24040. .24808
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="HERVL repeat: matches 3020. .3198 of consensus"
45756. .45854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43968. .43995 therefore matches 1. .709 of fincte="7 copies 4 mer tgtg 96% conserved 4350. .44381 therefore 2 mer at 93% conserved 4397. .44493 note="HBRV16 repeat: matches 2566 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14979. .45156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MLT1F repeat: matches 4. .541 of consensus"
         note="L1M4 repeat: matches 4110.
2868. .52899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 20. .141 of consensus" 9167. .39460
note="Alusx repeat: matches 9. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 332. .510 of consensus" 5044. .35456 note="MLT2FB repeat: matches 1. .413 of consensus"
                                                                      note="AluSg/x repeat: matches 129. .302 of consensus"
                                                                                                                                                                                                                                                                           note="HERVL40 repeat: matches 1380. .1617 of consensus" 6979. .49348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER44 repeat: matches 474.
2405. .32952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="19 copies 2 mer aa 78% conserved"
1773. .31867
                                                                                                                                                             note="LTR40b repeat: matches 4. .458 of
                                                                                                                                                                                                                                                  note="HERVL40 repeat: matches 2050. .4496 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8474. .38589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="50 copies 2 mer gt 68% conserved" 7595. .37800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7492. .37591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6974. .37277
note="AluJo_repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1MB1 repeat: matches 5495. .6052 of consensus"
2954. .33113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MADE1 repeat: matches 8. .80 of consensus"
                                                                                                                note="L2 repeat: matches 2535. .2748 of consensus"
                                                                                                                                                                                                          note="HERVL40 repeat: matches 5352. .5530 of consensus"
                                                                                                                                                                                                                                                                                                                                             note="HERVL40 repeat: matches 1124. .1351 of
                                                                                                                                                                                                                                                                                                                                                                                          note="LTR41 repeat: matches 3. .102 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L2 repeat: matches 2082. .2310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 1. .120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER44 repeat: matches 1. .96 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MLT1B repeat: matches 1. .389 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="7 copies 4 mer atag 92%
7432. .27509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33. .42581
_e="MER67C repeat: matches 1. .709 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="MER58A repeat: matches 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .31678
                                                                                                                                          .50815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .35916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 7. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 2566. .2674 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .724 of consensus"
                            .4231 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .224 of consensus"
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Submitted (16-M06-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone syl, 2002 this sequence version replaced gi:20268901.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations corresponding to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with mail overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
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S0828 bp DNA linear VRT 16-AUG-200
Schraftsh DNA sequence from clone BUSM1-6A2 Contains a novel gene
similar to CGFR, a novel OGFR pseudogene, two pseudogenes on a
novel LINE-like transposon, a novel reverse transcriptase
speudogene, the fez gene for forebrain embryonic zinc-finger
procein, part of a novel gene for a protein similar to Ca2+
dependent activator and four CpG islands, complete sequence.
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 80828)
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HTG; Ca2+ dependent activator; CpG island; fez; forebrain; OGFR;
opioid growth factor receptor; transposon; zinc-finger protein.
zebrafish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69212 TCTCTTAAGAGAGGTCCCAATCTCTTAACTCCTGGCAACTACTAATTTGTTATTCATGTC 69271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69272 TACAATTGCAGTATTAGAAGAACATATATAATTTAATTACATAATATGTAACTGTTTGT 69331
                                                                                                                                                                                                                                                                                                    note="LIMA9 repeat: matches 5549. .6270 of consensus"
                                                                                                                                                                                                                                                                                                                              62138. 62198
/note="L1MA9 repeat: matches 5317. .5375 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1MA9 repeat: matches 4826. .5309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTG 419
/note="16 copies 2 mer gt 93% conserved"
54804. .54928
/note="L2 repeat: matches 1714. .1838 of consensus"
55708. .55771
                                                                                                                                                                                                                                   'note="LTR33 repeat: matches 48. .398 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="FLAM A repeat: matches 2. .131 of consensus"
62687. .63166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 TATAATTAGAGAGGATGCATGGATATAATAAATAAGTAAAAGCTACGGTATCACCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluY repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.8%; Score 38.4; DB 9; Length 159919; Best Local Similarity 55.4%; Pred. No. 9.1; Matches 72; Conservative 1; Mismatches 57; Indels 0;
                                                                                                                                                           note="16 copies 4 mer tatg 78% conserved"
18435. .58781
                                                                                                                                                                                                                                                                        61425. .62137
                                                                                                                                                                                                                                                                                                                                                                                                             62544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 GATGATTTTY 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct
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LOCUS
DEFINITION
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROT; Tr.: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                   Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml his clone was isolated from a PAC library (Incyte Genomics, Inc.) and provided by G. Levkowitz (Genentech Inc., San Francisco, USA). This sequence is the entire insert of clone BUSM1-6A2 The true left end of clone BUSM1-13 is at 44958 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACACTGCATATACATAAACTTGATGCATGCAAACAC 149% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1338. 1405
/note="Dr000340 repeat: matches 120. 187 of consensus"
                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep BUSM1-6A2 is
from a Zebrafish PAC library
VECTOR: pCYPAC-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="3.4 copies 14 mer TACACATACATACA 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187. 709
hote="1.9 copies 12 mer TACTTAAAATAC 46% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158. 477
note="2.0 copies 10 mer AGTTTTACAT 40% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="2.8 copies 9 mer CATTATTAT 34% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               856. .874
/note="2.1 copies 9 mer TTGTGACTT 38% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="2.0 copies 8 mer TTAAAATA 32% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   653. .666
/note="2.0 copies 7 mer TACAAAA 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="2.4 copies 7 mer ATAAAAT 25% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1096. .1107
/note="2.0 copies 6 mer CATACA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2935. .2946
/note="2.0 copies 6 mer CATATA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="2.0 copies 6 mer CATATA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copies 6 mer GTCTCA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="2.0 copies 6 mer CATATA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="2.2 copies 5 mer AACAG 22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541. .557
/note="4.2 copies 4 mer AAAT 34% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101. .1133
/note="8.2_copies 4 mer ACAT 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies 4 mer TTTG 22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138. .160
/note="7.7 copies 3 mer ATT 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1782. 1799
Morce="180" Oopies 1 mer A 36% conserved"
1815. 1826
/note="2.0 copies 6 mer GTCTCA 24% conserv
                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          787. .2950
note="4.1 copies 40 mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/db xref="taxon:7955"
/clone="BUSM1-6A2"
                                                                                                                                                                                     --- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                             Contact: zface@sanger.ac.uk
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                     /note="Tandem repeat. Inconsistency in the number of copies of the repeat element between subclones." 6542. .6575
/note="2.1 copies 16 mer ATTTATCAAAGTGTGA 68% conserv
                                                                                                                  /note="Dr000340 repeat: matches 81. .207 of consensus" complement(6449. .6538) /note="Dr000340 repeat: matches 117. .207 of consensus"
                                                                                                                                                                                                                           6157. .6187
/note="7.8 copies 4 mer ACAT 62% conserved"
complement(6187. .6391)
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complement(4075. .4252)
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.="2.0 copies 7 mer TACAAAA 28% conserved"
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Submitted (13-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
4 (bases 1 to 126118)
Waterston,R.H.
Waterston,R.H.
       Direct Submission Submitted (09-MAR
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Submitted (16-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston,R.
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The sequence of Homo sapiens BAC clone RP11-182K3
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Sulston, J. E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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(09-MAR-2002) Department of Genetics, Washington
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/note="2.0 copies 6 mer CATATA 24% conserved"
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/note="2.0 copies 8 mer TTAAAATA 32% conserved"
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Pred. No. 11;
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note="similar to Bos taurus EST BE810028 (NID:g10241140)"
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                                               7525. .7604
/note="similar to Bos taurus EST BI680079 (NID:g15632987)"
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13841. 14227
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13884. .14235
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//note="match to EST BEB11024 (NID:g10243258)"

10204. .10325

//note="match to EST BEB11026 (NID:g10243260)"

10207. .10361
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/note="match to EST BEB11072 (NID:gl0243306)"

10223. 10361

/note="match to EST AL517947 (NID:gl2781440)"

(0319. 10361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match to EST BG983142 (NID:g14385864)"
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.0204. .10361
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(0204. .10361
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                                                                                                                                                                                                                                             3473. .8926
/note="match to EST BF935807 (NID:g12353131)"
      /525. .7604
/note="match to EST BI859737 (NID:g16000484)"
                                                                                                                                                                           'note="match to EST AU134477 (NID:g10995016)"
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'note="match to EST AL037954 (NID:95407270)"
.0204. .10361
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/note="match to EST AA328955 (NID:g1981442)"
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/note="aimilar to Mus musculus BST BB615821
(NID:g16456044)"
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10213. 10325
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/note="gimilar to Mus musculus EST BB615821
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1736. 12024
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1467. .11735
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|/rpt_family="MER2_type"
|2614. | 12774
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13615. .13994
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/rpt_family="AT_rich"
8473. .8926
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13162. .13187
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2027. 12481
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13003. 13026
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9379. .9665
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Feb 16, 2002 this sequence version replaced gi:18250125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-252K7, 2000 bp overlap.
Actual start of this clone is at base position 106699 of
RP11-252K7; actual end is at base position 126118 of RP11-182K3.
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/note="match to EST BE926756 (NID:g10452832)"
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'note="match to EST AL037617 (NID:95928218)"
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note="match to EST AL037954 (NID:95407270)"
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                      Center project name: H_NH0182K03
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/chromosome="2"
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1892. .1918
/rpc_family="(A)n"
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/note="match to EST
7525. .7604
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1. .126118
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rpt_family="MaLR"
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605_ foor
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7525. 760
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Search completed: January 12, 2003, 08:14:38 Job time: 3376 secs
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18084. .18129
/rpt_family="(TCTA)n"
18691. .18712
/rpt_family="AT_rich"
19094. .19636
/note="match to EST AL037616 (NID:g5928217)"
19686. .19709
/rpt_family="AT_rich"
19804. .19825
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/rpt_family="(A)n"

14438. .14799

/note="match to EST R82015 (NID:g858618) yj06f08.rl"

15005. .15305

/rpt_family="Alu"

17481. .17958

/note="match to EST BF771506 (NID:g12119406)"

17786. .18083

/_note="match to IST BF771506 (NID:g12119406)"
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Listing first 45 summaries
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Perfect score:
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    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAT88851
ABL15860
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ABL29368
AAL28368
AAX84302
AAK84300
AAK84301
ABL34024
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                                                                                      Drosophila melanog
Drosophila melanog
Human immune syste
Human chemically t
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                      Human
                                           Human immune/haema
                                                                 Human
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immune/haema immune syste
                                                               immune/haema
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Staphylococcus epi DNA transcription Human G-protein co	ABN92473 ABK28346 AAS16913	24 24	1422 8440 11046	ი ი ი 	32.2 32.2	443 454
Human Human	ABK83568 AAI83912	24 22	201143 397		32.4 32.2	41 42
CDNA	AAT41852	17	9789		N	40
Probe Human	AA139099 ABS08145	2 2	463 463		32.4	9 8
Probe		22	463		. 20	37
Human	AAK33310	22	463		Ν.	36
Human	AAK07518	22	463	•	2	35
Probe	ABA28022	22	463	•	2	34
Human	ABA59299	22	463		N	33
DNA transcription	ABK28430	24	17142			32
Human	ABL34107	24	17142	•	۲.	31
Chemically pretrea	AAS45498	22	17142	•	2	30
Human	AAD28377	24	6041			29
Human	ABK40061	24	13784			28
Arabidopsis	AAC48974	21	11220	6.7	ν.	27
Human	ABL32737	24	5497	6.7	ν.	26
Human	AAI84087	22	402	6.7	2	25
Genomic	AAF28545	22	62909	6.7	ω ω	
Human	ABA15292	22	8846	6.7	ω	23
Human	ABK84795	24	139389	. 7	33.2	22
Drosophila	ABL30286	23	4936	6.7		21
Pneumococcal	16	24	75		Ü	20
Human	AAK79382	22	25577		L	19
Human	2	22	(n	6.8		18
Streptococcus	AAV52192	19	9223		'n	17
Iron		24	777		w.	16
Drosophila	ABL03306	23	7978	6.9	34	15
EST	AAV87102	20	374	-	4	14
Human	AAX82876	21	179	7.1		13
Human	78	21		7.1	4	12
Signal	315	24	38342	7.1	5	11
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RESULT 1 AAT88851

AAT88851 standard; cDNA; 480

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mat_peptide
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                                                                                                                                            Macadamia integrifolia.
                                                                                                                                                                                     cDNA for Macadamia integrifolia antimicrobial protein 1.
      31-JAN-1996;
                      31-JAN-1997;
                                      07-AUG-1997.
                                                     WO9728185-A1.
                                                                                                                                                            Antimicrobial protein 1; growth inhibition; fungus; bacterium; fungi; bacteria; pathogen control; ss.
                                                                                                                                                                                                     27-MAR-1998 (first entry)
      96AU-0007802
                      97WO-AU00052.
                                                                            /*tag= b
148..375
/*tag= c
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70..147
                                                                     /product= antimicrobial_protein_1
                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                           61 ACCTCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATA 120
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                  1 ATTANGTETTTGAGTETCATACATACTETETECTCECCCACCATTAGCACTTATCAGETA 60
                                                                                                                                                                                                                     9
                                                                                                            The present sequence encodes Macadamia integrifolia antimicrobial protein 1, which exerts inhibitory activity on the growth of fungiand bacteria. It can be used for the control of pathogens in plants
                                                              New anti-microbial protein from Macadamia integrifolia - active in inhibiting the growth of fungi and bacteria in plants and animals
                                                                                                                                                                                                                     1 ATTAAGTCTTTGAGTCTCATACATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTA
                                                                                                                                                                                                                                                                    ACCTCAGCCATGCCTTCCACCAAGTTCTTCTCAGTCATTACTGTGATGATGCTCATA
                                                                                                                                                                                                                                                                                                           421 ATAATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGTG
                                                                                                                                                                                                                                                                                                 121 GCAATGGCAAGTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGT
                                                                                                                                                                                                                                                                                                                                      AACAACCGTGCTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                           241 TATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGCTGGATGCAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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                  Marcus JP;
                                                                                                                                                                                Length 480;
                                                                                                                                                                                                  0; Indels
                                                                                                                                                              Sequence 480 BP; 129 A; 103 C; 108 G; 140 T; 0 other;
                  Harrison SJ, Manners JM,
                                                                                                                                                                               97.4%; Score 480; DB 18; I
100.0%; Pred. No. 1.1e-142;
iive 0; Mismatches 0;
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 24; 38pp; English
                                                                                                                                                                                                    Conservative
                 Green JL,
                                   1997-448317/41.
                                                                                                                                                                                          Local Similarity
                                            P-PSDB; AAW31738
                  Goulter KC,
                                                                                                                                            animals.
                                                                                                                                                                                                  Matches 480;
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Best Local 9
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2189 idcgiadaaracaacrccgricagaracraarararaaracrirraaaaacarararrig 2130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 42062; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4667 BP; 1342 A; 1037 C; 954 G; 1334 T; 0 other;
                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grarrrrarggaarararraa 2047
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ID ABL15850 standard; cDNA; 5823
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                                                           23-MAR-2001; 2001WO-US09231.
                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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pharmaceutical; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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P-PSDB; ABB71757.
                                                                                                                                                                                                                       (PEKE ) PE CORP NY
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27-SEP-2001
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11-JUL-2000; 2000US-0614150

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 42056; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
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                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipscriatic;
                                                                                                                                                                   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
              02-JUL-2001; 2001WO-EP07537
                                                                                                       Homo sapiens.
                                                                                                                                                     neurofibromatosis;
                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                      ABL32078 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348
                                                                          WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATTTTATGGAATATATTTAA 3203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATCACCATGTGATGATTTTYA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGTAGAATACAACTCCGTTCAGATACTAAATATAATAACTTTTAAAAAACATATATTTG 3286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%;
53.1%;
                                                                                                                                                      rheumatoid arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.8; DB Pred. No. 1.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Indels
                                                                                                                                                                                                                                                                               51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5823;
                                                                                                                                                      epilepsy;
bowel disease
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ID AAD283
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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, eppliepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8011 BP; 1986 A; 145 C; 1776 G; 4104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 51; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-1032529:
01-SEP-2000; 2000DE-1043826:
                                                                                                                                                                                                                                                                                              Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD28368 standard;
                                                                                                                   30-JUN-2000; 2000DE-1032529: 01-SEP-2000; 2000DE-1043826:
                                                                                                                                                                                                                                                                                                                                                                            Human chemically treated genomic DNA #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD28368;
                                                                                                                                                              02-JUL-2001; 2001WO-EP07540
                                                                                                                                                                                              10-JAN-2002
                                                                                                                                                                                                                          WO200202809-A2
                                                                                                                                                                                                                                                       Homo sapiens.
                            WPI; 2002-154759/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 ATAATTAGAGAGATGCATGGATATAATAAATAAGTAAAAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y Match 7.2%;
Local Similarity 58.5%;
                                                                                                                                                                                                                                                                                   abuse; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTAAATTTAACCCAAATCTACCTAAATCCAAAACCCATCTTTAATCTTTTCAATATA 3088
                                                                                       EPIGENOMICS AG
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                                                         Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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0

Novel nucleic acid useful

for diagnosis and

therapy

of behavioral

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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also betalates to oligonuclectides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human and schizoaffective patients, and suicidal behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPS). The present sequence is human chemically treated genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3147 Archaattraacccaaarcraactaariccaaaacccarcritraarcrarara 3088
disorder, neurological disorder and cancer, comprises a sequence of a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGT 420
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 35.6; DB 24; Length 8011;
Best Local Similarity 58.5%; Pred. No. 2.3;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 8011 BP; 1986 A; 145 C; 1776 G; 4104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 ATAATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTAC 466
                                                                          Claim 1; Page 56-60; 190pp; English.
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24-FEB-2000; 2000US-0184664.
16-MAR-2000; 2000US-0184580.
16-MAR-2000; 2000US-0184580.
17-MAR-2000; 2000US-019123.
19-AFR-2000; 2000US-02515.
07-JUN-2000; 2000US-020467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-021135.
07-JUL-2000; 2000US-0216880.
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2000US-0217496.
2000US-0218290.
2000US-0220963.
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26-JUL-2000;
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2000US-0225213.
2000US-0225214.
2000US-022526.
2000US-022526
2000US-022526
2000US-0225270.
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2000US-0225758.
2000US-0225759,
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2000US-0229343.
2000US-0229344.
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2000US-0229509.
2000US-0229513.
2000US-0230437.
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2000US-0231968.
2000US-0232397.
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2000US-0231242.
2000US-0231243.
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2000US-0233063.
2000US-0233064.
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2000US-0234274.
2000US-0234997.
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2000US-0236367.
2000US-0236368.
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2000US-0236370.
2000US-0236802.
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2000US-0232399
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                                14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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                                                                                                    22-AUG-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleocides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For c example, they may be used to treat disorders associated with decreased expression by recttifying mutations or delations in a patient's genome c that affect the activity of (I) by expressing inactive proteins or to c supplement the patients own production of (I). Additionally, (I) c polynucleotides may be used to produce the secreted (I), by inserting c the nucleic acids into a host cell and culturing the cell to express the correctin. (I) proteins and polynucleotides may be used to prevent, c diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
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08-NOV-2000

08-NOV-2000

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08-NOV-2000;
08-NOV-2000;
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                                                                                                                                                                                                                                    NUCLEIC acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                     Disclosure; SEQ ID NO 39114; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                       WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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2000US-0246477.
2000US-0246478.
2000US-0246523.
2000US-0246523.
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2000US-0249216.
2000US-0249217.
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2000US-0246613.
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2000US-0249300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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07-JUL-2000;
07-JUL-2000;
       14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39112
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28-JUN-2000;
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18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                           2000US-0224519.
2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225267.
2000US-0225268.
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2000US-0224518.
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2000US-0217487.
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2000US-0215135.
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Pred. No. 2.7;
0; Mismatches
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20-OCT-2000; 2000US-0241221.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
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20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-024182.
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14-AUG-2000;
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23-AUG-2000;
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2000US-0249209
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2000US-0250160.
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                     17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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                                                                        17-NOV-2000;
17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39112; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
acituity, and can be used in gene therapy and vaccine production. (I)
acituity, and can be used in gene therapy and vaccine production. (I)
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cytostation by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
cytostation by rectifying mutations of (I). Additionally, (I)
cytostation by be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
cytotein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AK64703
cc to AAK87694 represent human immune/haematopoietic antigen genomic
c sequences from the present invention. AAK5492 to AAK6750 and AAM82169
xx

Sequence 8209 BP; 2721 A; 1260 C; 1380 G; 2848 T; 0 other;

0; Gaps Query Match 7.2%; Score 35.4; DB 22; Length 9209; Best Local Similarity 55.2%; Pred. No. 2.7; Matches 69; Conservative 0; Mismatches 56; Indels 0;

345 TITIGGINGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTC 404

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RESULT 8
AAK84301
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          2000US-0179065.
2000US-0180628.
2000US-0180628.
2000US-0189874.
2000US-0198123.
2000US-029467.
2000US-0214886.
2000US-0214886.
2000US-0216135.
2000US-0216135.
2000US-0216135.
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2000US-0217487.
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2000US-0228213.
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2000US-0232400

2000US-0232401

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2000US-0230437.
2000US-0230438.
2000US-0231242.
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2000US-0241221.
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ABL34024

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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)

c amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (II)
correction and polynucleotides may be used in the prevention, diagnosis and
ct reatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
c expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
c that affect the activity of (I) by expressing inactive proteins or to
c supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting
cc the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
c protein. (I) proteins and polynucleotides may be used to prevent,
c diagnose and treat immune/haematopoietic-related diseases, especially
cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703
cc cancers and cancer metastases of haematopoietic antigen genomic
c to AAK87694 represent human immune/haematopoietic antigen genomic
c represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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Best Local Similarity 55.2%; Pred. No. 2.7;
Matches 69; Conservative 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8210 BP; 2722 A; 1260 C; 1380 G; 2848 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
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05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 3
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukeamia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.1%; Score 35.2; DB 24; Length 6375; 5.8%; Pred. No. 2.7;
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                                                                                                          Human immune system associated gene SEQ ID NO: 1997.
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ABL34024 standard; DNA; 6375 BP.
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01-SEP-2000; 2000DE-1043826.
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Best Local Similarity 55.89
Matches 67; Conservative
                                                                          (first entry)
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                                                                          26-MAR-2002
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derived chemically modified sequence #469.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid comprising a sequence of 18 cc bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for assertaining genetic and/or epigenetic parameters for the diagnosis of diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the creates serving as basis for diagnosis and/or prognosis events which care disadvantageous to patients. The present sequence is one of the parameters and compared to another set of genetic and/or spigenetic parameters, the compared to another set of genetic and/or spigenetic parameters may be a proposed to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic parameters and the compared to another set of genetic and/or spigenetic paramete
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                        Sequence 38342 BP; 11153 A; 472 C; 7565 G; 19152 T; 0 other;
                                                        2301 TTATAAAAATGTTTTTTTTTÄGATAAATTTÄTTTÄATAAAATÄGÄTTÄTTTÄÄÄGÄTA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                       406
                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 469; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine
                                                                                                                                                                                                                                                                                       Local
                                                                                                       TITGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCT 405
                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1013847.
                                                                                                                                                                                                                                                                                  7.1%;
55.8%;
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                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                     Score 35.2; D. Pred. No. 6.8;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                         Length 38342;
                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                           CC signal transduction associated genes. The DNA sequences are chemically C modified using a solution of bisulphite, hydrogen sulphite or Cd disulphite. Also disclosed are oligonuclectides and/or PNA oligomers CC for detecting the cytosine methylation state (CpG islands) of these CC genes, and a method for the diagnosis and/or therapy of genetic and CC epigenetic parameters of genes associated with signal transduction. CC The genomic DNA can be obtained from cells or cellular components which CC contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, CC cerebral-spinal fluid, tissue embedded in paraffin such as tissue from CC eyes, intestine, kidney, brain, heart, prostate, lung, brasst or liver, CC ciscases associated with signal transduction e.g. solid tumours and CC diseases associated with signal transduction e.g. solid tumours and CC cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA CC sequences of different genes associated with signal transduction, or their romalementary emembersa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK31506
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                           Sequence 38342 BP; 11153 A; 472 C; 7565 G; 19152 T; 0 other;
                                                                                                                                                                                                                                                         their complementary sequences.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic
                                                                                                  346 TTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCT 405
                                                                                                                                                                                                                                                      European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to chemically modified DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 349; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-147896/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529; 01-SEP-2000; 2000DE-1043826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction associated gene modified DNA #175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001; 2001WO-EP07472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200926-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK31506 standard; DNA; 38342
                                                                                                                                                               Local Similarity
                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                              Conservative
                                                                                                                                                             7.1%;
55.8%;
                                                                                                                                            0
                                                                                                                                                       Score 35.2; DB 24;
Pred. No. 6.8;
                                                                                                                                        Mismatches
                                                                                                                                          53;
                                                                                                                                                                            Length 38342;
                                                                                                                                          Indels
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                                                                                                                                        Gaps
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The present invention describes an isolated dysferlin DNA of 20-25

Tucleotides in length, comprising a nucleotide sequence specifically selected from nucleotides 11-913, 929-948, 1019-1038, 1392-1411, 1014-1038, 1392-1411, 1014-1038, 1398-1317, 1352-1371, 1241-1433, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 1714-1734, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-1739, 1714-17
                                                                                                                                                                                                                                       Human; dysferlin; mutant; identification; chromosome 2p12-14; detection; muscular dystrophy; diagnosis; hereditary muscular dystrophy; miyoshi myopathy; limb girdle muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dysferlin polynucleotide, its mutant form useful for diagnosis and treatment of hereditary muscular dystrophies e.g. miyoshi myopathy and limb girdle muscular dystrophy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 34.8; DB 21; Length 179;
65.4%; Pred. No. 0.6;
tive 0; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 CATACTCTTCTCCCCCACCATTAGCACTTATCAGCTAACCTCAGCCATGGCTTCCACC 81
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                                                                                                                                                                                          Human dysferlin related nucleotide sequence SEQ ID NO:43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chou F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 101; 136pp; English.
                                            AAA36785 standard; DNA; 179 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown RH, Liu J, Hoffman E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US19394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0097930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                03-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-246531/21.
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200011016-A1.
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-AUG-1998;
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                                                                                                   AAA36785;
RESULT 12
                          AAA36785/
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This invention describes a novel human dysferlin nucleic acid (I) and its encoding protein (II), which has anti-dystrophic activity and can be used for gene therapy. Introduction of (I), a vector comprising (I) or dysferlin into a cell of a mammal can be used to decrease the symptoms of muscular dystrophy. The dysferlin gene is normally expressed in skeletal hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle muscular dystrophies, e.g. Miyoshi myopathy and limb girdle muscular dystrophies and oligonucleotides derived from (I) can be used in diagnosis of or risk identification for dysferlin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders in patients, fetus, or pre-embryos. Expression of brain-specific dysferlin may be important as a marker for normal neural development. Dysferlin DNA or subgenomic coding sequences can be used for therapy of the hereditary muscular dystrophies. This sequence represents a fragment of the human dysferlin gene described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel dysferlin genes and related proteins useful for diagnosis, risk identification and treatment of hereditary muscular dystrophies and other dysferlin related disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                  Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human; skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis; limb girdle muscular dystrophy-2B; brain-specific; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Score 34.8; DB 21; Length 179; larity 65.4%; Pred. No. 0.6; Conservative 0; Mismatches 27; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 179 BP; 42 A; 34 C; 66 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 111; 146pp; English.
                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0097927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US19395.
                                                                                                                  AAX82876 standard; DNA; 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AAGTICTICTTGTTACTC 78
95 AAGTTCTTCTTGTTACTC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                            30-JUN-2000 (first entry)
                                                                                                                                                                                                                                  Human dysferlin DNA #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-237646/20.
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                                                                                                                                                                                                                                                                                                                                                                                        WO200011157-A1.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999;
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                                                                                                                                                        AAX82876;
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RESULT 14 AAV87102

82 AAGTTGTTCTTCAGTC 99

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RESULT 15
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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemastopoiesis regulating activity, tissue growth activity, haemostatic activity haemostatic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                         and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                               Sequence 374 BP; 132 A; 69 C; 48 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an expressed sequence tag polynucleotide of the invention. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 453; 633pp; English.
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                                                                                            AAGCTACGGTATCACCATGTGATGATTTTYACCC
                                                                                                                                                                                                                     AACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCA 399
                                                                                                                                                               AATGCTTTTTAAAGGAAAAAAACATGAAATCAAATAATAGATTT-TCACTTAATTCAATTT 269
                                                                          GAAGTACAGAATTCCCATATAATCACTTTTCCCC
                                                                                                                                      TTTGTTTTGTTTTAATTTTCAATTACTAGACAGATCTAGGTTTATAAAAGAACTAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Spaulding
                                                                                                                                                                                                                                                                   Conservative
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55.2%;
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Treacy M;
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                                                                                                                                                                                                                                                                Score 34.4; DB Pred. No. 1.2; 1; Mismatches
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ABL03306 standard; cDNA;

Search completed: January 12, Job time : 284 secs

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Matches
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; development pharmaceutical; gene;
                                                                                                                                                                                                           Sequence 7978 BP; 2487 A; 1370 C; 1394 G; 2727 T; 0 other;
                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4400; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
P-PSDB; ABB59203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE
                                                                                                                                                                                                                                                                                        ABB57737-ABB72072)
                                                                                                                                                                Match 6.9%;
Local Similarity 50.6%;
                                                                                                                      CCAGGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAAC 388
 TARATAAGTAARAGCTACGGTATCACCATGTGATGATTTTYA 490
                             TCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAGAGATGCATGGATATATAA 448
                                                                                        CAAGGGGCACCTCCGCTTTTCGTGGTTATCAATGCCTAAGCCATTGAAATATTATTATTAT 7243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
cal; gene; ss.
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid detection reagent for detecting 1000 or more and for elucidating cell signalling and cell-cell
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Pred. No. 7.4;
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                                                                                                                                                  Mismatches
                                                                                                                                                                              DB 23;
                                                                                                                                                   80;
                                                                                                                                                                            Length 7978;
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Maximum Match 100%
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Perfect score:
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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493
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match Length
 6.8 9223
6.5 1422
6.5 537
6.4 6354
6.4 246240
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6.3 12135
6.2 13115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
 US-08-961-527-59
US-09-134-001C-1936
US-09-134-5-399-5
US-09-058-389A-5
US-09-058-389A-2
US-09-058-394A-21
US-08-724-394A-21
US-08-724-394A-22
US-07-741-453A-57
US-08-121-446-3
US-08-121-446-3
US-09-600-776-9
US-08-973-462-2
US-08-973-462-1
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US-08-98-627-28
US-08-99-020-818-4
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Sequence 59, Appl
Sequence 5, Appli
Sequence 5, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 27, Appli
Sequence 37, Appli
Sequence 37, Appli
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Sequence 47, Appli
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Sequence 28, Appli
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4. Appli 2. Appli 11. Appli 11. Appli 12. Appli 13. Appl 22. Appli 14. Appli 13. Appli 11. Appli 11. Appli 11. Appli 12. Appli 13. Appli 14. Appli 15. Appli 15. Appli 16. Appli 17. Appli 18. Appli 19. Appli 20. Appli 21. Appli 22. Appli 23. Appli 24. Appli 25. Appli 26. Appli 27. Appli
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LOCATION: 1.537
CTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.78
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Matches 69; Conservative
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                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                  TOPOLOGY:
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LENGTH: 537
TYPE: DNA
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Berler ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE DE INVENTION: EPIDERRIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: S674
LENGTH: 1422
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Sequence 5. Application US/08845539

CENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
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420 TATAATTAGAGAGATGCATGGATATAATAAATAAGTAAAAGCTACGGTATCACCATGT 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1172 AGATACAAATATAAATATAAACTAGGTAAAAGCTCTGTTCT 1132
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                US-09-134-001C-1936/c
; Sequence 1936, Application US/09134001C
; Patent No. 6380370
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25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bastian, Kevin L.
                                                                                                                                    4851 TGTGAAAGCTACC 4839
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
COMPUTER: IBM PC COMP
                                                                                           480 GATGATTTTYACC 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-001C-1936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Sequence 5, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit Specific and Ripening Regulation Expansin Genes
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
                                                                                                       238 GGCTATGACTTCAGCTACACTGGACAAACTGCTCTCTTACAACCAGGCTGGATGCAGT 297
                                                                                                                                                             82 GGCTATGGCGTCAACACAGCTGCTCTTAGTACTGCTTTCTTCAACAATGGCCTCAGCTGT 141
                                                                                                                                                                                                                   0; Gaps
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6.5%; Score 31.8; DB 2; Length 537; 52.7%; Pred. No. 0.88; .ive 0; Mismatches 62; Indels (
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LOCATION: (1)..(537)
OTHER INFORMATION: melon expansin (CmEx1) partial CDNA clone
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202 TGTATCTTCAT

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RESULT 6
US-09-611-781-5
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-143-1684
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                      5639 CACCCTGTCCGTCTTCCCCCCCATCACAGCCATGGTGACCAGCTCCACCAGTCCTGGGAA 5698
                                                                                                                                                                   5699
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pair
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
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TITLE OF INVENTION: A. TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/058,389A
FILING DATE: APRIL 9, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                 78 CACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCAATGGCAAGTGAGAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                        TGGACAAACTGCTGCTCTTACAACCAGGCTGGATGCAGTGG 299
                                                                                                                                                                                                         ATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCAGCTACAÇ 257
                                                                                                                                                                                                                                                      AACCCCATCTGCTGCTTCCTCCTCTTCAACATCATGGACTGG 5860
                                                                                                                                                                                                                                                                                              GGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCG 197
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                               US-08-724-394A-20/c
                                                       RESULT 7
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Sequence 20, Application US/08724394A Patent No. 5872237
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Patent No. 6423829
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/058,389
FILING DATE: April 9, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Patel, Di
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 6354 base pairs
                                                                                                          5819 AACCCCATCTGCTGCTTCCTCCTCTTCAACATCATGGACTGG 5860
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                       198 ATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCAGCTACAC 257
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                                                                                                                                                                                   GTGGAGTGAGTGTCAGGGTGGAGAAGACGGCAGGGGGGGTACAAAGGGGAAGACG
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N: A NITROBENZYLMERCAPTOPURINERIBOSIDE
N: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
N: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
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                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.6; DB 4;
Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6354;
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COUNTRY:
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                                                                                                                                                                         TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 144916 TTCACAATGGATAAACACGTGTAATATACCTCC 144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitte, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ 1D NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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50.3%; Pred. No. 28;
tive 0; Mismatches
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| LOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG'
US-08-724-394A-20
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US-08-724-394A-21/C
US-08-724-394A-21/C
Sequence 21, Application US/08724394A
Patent No. 5872237
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.
                                                                                                          Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: cDNA
                       Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.3
Matches 77; Conservative
GENERAL INFORMATION:
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131 GTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTG 190
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6.4%; Score 31.4; DB 2; Length 246240;
Best Local Similarity 50.3%; Pred. No. 28;
Matches 77; Conservative 0; Mismatches 76; Indels 0;
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: STREET: CA
STATE: CA
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Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 144916 Trcacaariggaraaacacgreraararaccrec 144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  017957-000100
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10S-08-724-394A-22/c
; Sequence 22, Application US/08724394A
; Parent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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APPLICANT: Feder,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: 1.246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                 US-07-741-453A-57/c
                                                                                                                                                                                                                                                                                             Sequence 57, Application US/07741453A Patent No. 6228597
GENERAL INFORMATION:
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Best Local Similarity 50.3%;
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                         APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
NUMBER OF SEQUENCES: 62
NUMBER OF SEQUENCES: 62
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 CTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 GTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTG 190
                                   STREET: 1615 L STREET, N.W. CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant TOPOLOGY: not relevant
                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 01-OCT-1996
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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20036
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US-08-121-446-3/c
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
LENGTH: 4417 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08121446 Patent No. 6313276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
SOTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,446
FILING DATE:
CLASSIFICATION: 435
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        APPLICANT: IMURA, HIROO
APPLICANT: NAKAO, KAZUWA
APPLICANT: NAKANISHI, SHIGETADA
TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
NUMBER OF SEQUENCES: 4
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REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Disk
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                 CITY: Palo Alto
                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4417 base pairs
TYPE: NUCLEIC ACID
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                       94304-1018
                                                                                                                                                                                                                            California
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Db 106735 ACAGGCATAAAATATATATATATACTTAAAACCAAGGTTTTCA 106693
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APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE REPERENCE: CL000968
FILLE REPERENCE: CL000968
FULLE EPERENCE: CL000968
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6.3%; Score 31; DB 4; Length 112132;
Best Local Similarity 56.3%; Pred. No. 26;
Matches 58; Conservative 0; Mismatches 45; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3%; Score 31; DB 4; Length 4301; Best Local Similarity 51.0%; Pred. No. 4.7; Matches 73; Conservative 0; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                   29900-20324.00
                                               APPLICATION NUMBER: US 07/911,684
FILING DATE: 10-07U-1992
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3553 AAGGGTATCAGGATGTAAAATT 3531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1) ... (112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
                                                                                                                                                                           NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 TACGGTATCACCATGTGATT 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
238..1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-741-150-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-121-446-3
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: MALBARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/973,462B
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER PILING DATE: 1996-06-12
EARLIER PILING DATE: 1995-06-13
NUMBER: OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2772 AGTGAGGCAAGAACACAGAGACACTGGACAAGCTACGGCAGGCGGTGACGGAGCTGTCT 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTGTTGTACAACCAGGCTGGAT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 ITCAICCAAIGCIAGAITICAIAACICIIGGAICCAICITCIAIGITTITCAAGIGIAIA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.2%; Score 30.6; DB 4; Length 5361;
Best Local Similarity 52.0%; Pred. No. 7.2;
Matches 66; Conservative 1; Mismatches 60; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.2%; Score 30.8; DB 4; Length 3715; Best Local Similarity 61.0%; Pred. No. 5.1; Matches 50; Conservative 0; Mismatches 32; Indels 0;
                                                                               GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PCT
CURRENT APPLICATION NUMBER: US/09/600,776
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: JP P1998-011434
PRIOR RILING DATE: 1998-01-23
PRIOR RILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08973462B
Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2832 GAACAGGTGCTGCAGATGCGAG 2853
                     Sequence 9, Application US/09600776
Patent No. 6326168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 GCAGTGGTGTTGCACACCCAG 314
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 5361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: P. falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1)..(5361)
US-08-973-462-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Rattus sp.
US-09-600-776-9
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SEQ ID NO 9
LENGTH: 3715
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US-08-973-462-2/c
6-914-009-60-SD
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Search completed: January 12, 2003, 08:42:01 Job time: 365 secs
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                                                                                5428 ATGTTTTAAATTCTTAAAGATATCAAATACAAATGAATAAAACGGTCTCTCCTTATTTTT 5369
                                                                                                                        5368 ÁTTTATÁ 5362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5184 ATGTTTAAATTCTTAAAGATATCAAATACAAATGAATAAAACGGTCTCCCTTATTTT 5125
                                                                                               424 ATTAGAGAGATGCATGGATATAATAAATAAGTAAAAGCTAACGGTATCACCATGTGATG 483
                                                                                                                                          364 TTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTTCAAGTGTATA 423
                                                             484 ATTTTYA 490
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
Published_Applications_NA:*

1: /cgn2_6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/2/pubpna/UCT_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*

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11: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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493
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	NO.	Score	Query Match	Query Match Length 99.9 493	10 Bg	ID US-09-882-434A-2
	N	32.4	6.6	463	10	US-09-864-761-6488
ი	ω	32	6.5	202001	10	US-09-734-674-3
ი	4	32	6.5	465237	10	US-09-933-267A-1
ი	ഗ	31.6	6.4	133	10	US-09-867-701-102
	6	31.4	6.4	224	10	US-09-960-352-953
n	7	31.4	6.4	614	10	US-09-764-864-168
ი	œ	31.4	6.4	638	10	US-09-764-864-604
ი	9	31.2	6.3	335913	9	US-09-754-853A-2
ი 	10	31.2	6.3	335913	9	US-09-754-853A-3
Ω	11	31	6.3	4301	10	US-09-931-157-2
Ω 	12	30.8	6.2	493	10	US-09-882-434A-
	13	30.8	6.2	3715	9	US-09-965-830-9
Ω 	14	30.6	6.2	453	9	US-09-929-230-3
	15	30.6	6.2	2203	10	US-09-739-907-39
ი 	16	30.6	6.2	5361	9	US-09-742-096-2
ი 	17	30.6	6.2	6152	9	US-09-742-096-1
	18	30.2	6.1	488	9	US-10-046-935-456
	9	ر د د	6.1			

45	44	43	c 42	41	c 40	39	c 38	c 37	36		c 34		32	c 31	c 30				26	25	c 24	23	c 22	21	20
29	29	29.2	29.2	29.2	29.2	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.6	29.6	29.6	29.6	29.6	29.6	29.8	29.8	30	30	30.2	30.2	30.2
5.9	5.9	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1
243	185	2000	1366	530	202	13341	10378	1808	1361	634	525	402	2000	467	262	216	216	216	1143	275	2830	450	2456	1873	939
10	10	ø	v	9	10	œ	10	10	10	10	10	10	ø	10	10	10	10	9	10	10	9	10	10	10	9
US-09-878-574-13309	US-09-878-574-11947	US-09-938-842A-3496	US-09-938-842A-3485	US-09-796-692-3253	US-09-969-373-380	US-08-910-386A-1	US-09-764-847-1938	US-09-925-297-192	US-09-764-864-218	US-09-879-536-825	US-09-919-580-735	US-09-954-456-2038	US-09-938-842A-3659	US-09-867-701-2045	US-09-878-574-11395	US-09-833-263-714	US-09-922-217-714	US-10-025-380-714	US-09-818-564-1	US-09-923-876-5512	US-09-900-714A-1	US-09-797-467-4	US-09-822-830A-114	US-09-925-301-238	US-09-938-842A-2062
Sequence 13309, A	Sequence 11947, A	Sequence 3496, Ap	Sequence 3485, Ap	Sequence 3253, Ap	Sequence 380, App	Sequence 1, Appli	Sequence 1938, Ap	Sequence 192, App	Sequence 218, App	Sequence 825, App	Sequence 735, App	Sequence 2038, Ap	Sequence 3659, Ap	Sequence 2045, Ap	Sequence 11395, A	Sequence 714, App	Sequence 714, App	Sequence 714, App	Sequence 1, Appli	Sequence 5512, Ap	Sequence 1, Appli	Sequence 4, Appli	Sequence 114, App	Sequence 238, App	Sequence 2062, Ap

ALIGNMENTS

```
APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: D9/117615
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1997-01-31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)...(375)
; OTHER INFORMATION: y=t or c.
US-09-882-434A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-882-434A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09882434A Patent No. US20020108144A1 GENERAL INFORMATION:
                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                    LENGTH: 493
TYPE: DNA
ORGANISM: Macadamia integrifolia
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밁 Ş Query Match 99.9%; Score 492.6; DB 10; Length 493; Best Local Similarity 100.0%; Pred. No. 1.6e-141; Matches 493; Conservative 0; Mismatches 0; Indels 0; ATTRAGTCTTTGAGTCTCATACATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTA 60 ATTAAGTCTTTGAGTCTCATACATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTA 60 0 Gaps 0

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61 ACCTCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATA 120

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LENGTH:
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION NUMBER: US 60/180, 312
PRIOR PLING DATE: 2000-02-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-36
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PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                      121 GCAATGGCAAGTGAGGTGAATGGAATGCATTTACAGTATGGAGTGGTCCAGGTTGT
61 ACCTCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATA
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                                                                                                   121 GCAATGGCAAGTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGT
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Patent No. US20020048763A1
GENERAL INFORMATION:
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APPLICANT: WEI, MING-Hui et al TILE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLOOLOIB CURRENT PAPLICATION NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

CONTRANT ELEMENT FILING DATE: 2000-12-13

LENGTH: 202001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 32.4; DB 10; Length 463; 60.0%; Pred. No. 2.4; tive 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: MAP TO AC003025.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
US-09-864-761-6488
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
SEQ ID NO 6488
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(202001)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity
Matches 59; Conserva
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US-09-734-674-3/c
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Db 150183 CTGAGTTTCTATGAATTCATTATATAACTAATTAATATATTAT 150140

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US-09-867-701-10265/c
; Sequence 10265, Application US/09867701
; Patent No. US20020132237A1
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 09/692414
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/768184
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 09/804076
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 09/826314
PRIOR APPLICATION NUMBER: 09/826314
PRIOR FILING DATE: 2001-04-05
                                                                                                         SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10265
LENGTH: 133
TYPE: DNA
ORGANISM: Homo sapien
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Best Local
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                                                 Query Match
                                                                                                                                                                                                                              APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/933,267A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/160626
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TITLE OF INVENTION: Bstrogen receptor alpha variants and
TITLE OF INVENTION: methods of detection thereof
FILE REFERENCE: CL000258CI4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-10-20
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  Local Similarity 56. hes 58; Conservative
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                      6.4%; Score 31.6; DB 10; 56.9%; Pred. No. 2.2;
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0; Mismatches
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44;
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                                              Length 133;
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APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITTLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9535
LENGTH: 224
TYPE: DNA
OTHER INFORMATION: Clone ID: 41-LIB3058-026-Q1-K1-C2
US-09-960-352-9535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 168, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9535, Application Patent No. US20020137139A1 GENERAL INFORMATION:
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                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ23 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                LENGTH: 614
TYPE: DNA
288 TGGATGCAGTGGTGTTGCACA 308
                                                              353 TCAGAGAGTTGGCTACAACTTCTGCTGCACTGAACACACTGGTAGGGTTTCTCCTCAGCA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 TTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAGAGAT-GCAT 438
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                                                                                                      228 TCAGAAGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 GGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGTGATGATTT 487
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TTTTATAAATTTTTATTTTATTTTCTAATTTTTCAAATTTÄÄÄÄTTTATTÄTTTTATCÄÄ 110
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Local Similarity 61.5%;
les 67; Conservative
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                                                                                                                                                       Conservative
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                                                                                                                                                   Score 31.4; DB Pred. No. 5.8; 0; Mismatches
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364 TTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATA 423
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LOCATION: (46798)..(48763),(48975)..(49573)

CTHEN INFORMATION: Clone ID: 240017_region_G3

US-09-754-853A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 185096 ATTTTT 185091
                                                                                                                                                                                                                                                        Db 185096 Arrirr 185091
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US-09-931-157-2/c
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Sequence 2, Application US/09754853A

PUBLICANT NO. US20030005491A1

GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)8

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR PAPLICATION NUMBER: US 60/174,880

PRIOR PLICATION NUMBER: US 60/174,880

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 2

LENGTH: 335913
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; LOCATION: (45163) .. (45314), (45450) .. (45509), (46941) .. (48763), (48975) .. (49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2
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6.3%; Score 31.2; DB 9; Length 335913;
Best Local Similarity 52.4%; Pred. No. 1.7e+02;
Matches 66; Conservative 1; Mismatches 59; Indels 0;
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6.4%; Score 31.4; DB 10; Length 638;
Best Local Similarity 61.7%; Pred. No. 5.9;
Matches 50; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223 CURRENT APPLICANT: NUCLEIC ACIDS, Proteins, and Antibodies FILE REFERENCE: PT223 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 604 LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (15)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (43)
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-604
                                                                                                                      ; Sequence 604, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
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293 TGGGTTTTCTGGTGTTCAATA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
                                                                                                      -09-764-864-604/c
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US-09-74-853A-3/c

| Sequence 3, Application US/09754853A |
| Sequence 3, Application US/09754853A |
| Sequence 3, Application No. US20030005491A1 |
| GENERAL INFORMATION: |
| APPLICANT: Hauge, Brian M. |
| APPLICANT: Parsons Jeremy D. |
| APPLICANT: Parsons Jeremy D. |
| APPLICANT: Parsons Jeremy D. |
| TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With |
| TITLE OF INVENTION: Soybean Cyst Nematode Resistance |
| TITLE OF INVENTION: Soybean Cyst Nematode Resistance |
| CURRENT FILING DATE: 2001-01-05 |
| PRIOR PELING DATE: 2000-01-07 |
| NUMBER OF SEQ ID NOS: 1119 |
| CONTROL OF SEQ ID NOS: 1119 |
| PRIOR FILING DATE: 2000-01-07 |
| PRIOR FILING DATE: 2000-01-07 |
| PRIOR FILING DATE: 2000-01-07 |
| PRIOR FILING DATE: 2000-01-07 |
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                                                                                                                                                                                                                                                                                     424 ATTAGAGAGATGCATGGATATATAATAAATAAGTAAAGCTACGGTATCACCATGTGATG 483
                                                                                                                                      424 ATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGTGATG 483
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APPLICANT: Imura, Hiroo
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakanishi, Shigetada
TITLE OF INVENTION: Human Endothelin Receptor
FILE REFERENCE: 299002032411
CURRENT APPLICATION NUMBER: US/09/931,157
CURRENT FILING DATE: 2001-10-15
PRIOR PLLING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: 07/911,684
PRIOR FILING DATE: 1992-07-10
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PRIOR APPLICATION NUMBER: 09/36/395
PRIOR FILING DATE: 1999-07-30
PRIOR PILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-11-09
PRIOR PELICATION NUMBER: 09/17/100052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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US-09-882-434A-2/c
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; LOCATION: (238)...(1566)
US-09-931-157-2
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Best Local (
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Best Local Similarity
Matches 73; Conserv
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APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Joddie Lyn
APPLICANT: Green, Joddie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
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PRIOR FILING DATE: 1991-07-12
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (70)...(375)
OTHER INFORMATION: y=t or c.
                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Macadamia integrifolia
                                                                                                                                                                                                                                                                                                        FEATURE:
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 493
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279 CAACCAGGCTGGATGCAGTGTTTGCACACACCTTTTGGGTCCAGTGCCAGGGCATG 338
                                                          364 AGATACTCTTCCAACCAAAAGGGTTGCATGCCCTGGCACTGGACCCAAACCTGGTGTGTG 305
                                                                                                 219 AGCTATACATCAGAAGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 TACGGTATCACCATGTGATGATT 486
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                                                                                                                                                                   Local Similarity
                                                                                                                                             74;
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50.7%;
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51.0%;
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                                                                                                                                             0; Mismatches 72;
                                                                                                                                                             Score 30.8; DB 10;
Pred. No. 7.8;
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                                                                                                                                                                              Length 493;
                                                                                                                                           Indels
                                                                                                                                        0; Gaps
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NAME/KEY: misc feature

NAME/KEY: misc feature

1. CCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57, 10CATION: 96, 69, 78, 81, 105, 111, 117, 123, 135, 141, 133, 162, 21, 10CATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222, 10CATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324, 243, 246, 258, 261, 270, 297, 306, 312, 324, 243, 245, 258, 261, 270, 297, 306, 312, 324, 10CATION: 30, 333, 336, 336, 351, 357, 360, 366, 372, 390, 393, 10CATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453, 07HER INFORMATION: n = A,T,C or G
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Matches 50; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 9
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APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PCT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/965,830
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 09/600,776
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
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6.2%; Score 30.6; DB 10; Length 2203;
Best Local Similarity 55.0%; Pred. No. 20;
Matches 60; Conservative 0; Mismatches 49; Indels 0; Gaps
                                                                                                                                                                                                                  64 TCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCA 123
                                                                                                                                                                                                                                                                                                                                                                                          265 CYTINARNCCDATCCACAINSWNGTRAAYIINARNGTYTGNSWNGCNARYIINCCNACRA 206
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Query Match
6.2%; Score 30.6; DB 9; Length 453;
Best Local Similarity 26.3%; Pred. No. 8.6;
Matches 67; Conservative 47; Mismatches 141; Indels
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TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: P2022P1
FILE REFERENCE: P2022P1
CURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR APPLICATION NUMBER: 00/070,567
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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LOCATION: (1846)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (1246)
OTHER INFORMATION: n equals a,t,g, or c
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Patent No. US20010012889A1
GENERAL INFORMATION:
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Search completed: January 12, 2003, 09:41:31
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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B1416519 hasp001xd
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                                                                                                                          AUTHORS
TITLE
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                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

B 1 (bases 1 to 605)

K Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.

The Pine Gene Discovery Project

Unpublished (1999)

Contact: Ross Whetten

Forest Biotechnology Group

North Carolina State University, 6113 Jordan Hall, Raleigh

NC, 27695-8008

Tel: 919-515-7800

Fax: 919-515-7801
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                        Email: rosswhet@unity.ncsu.edu
Seg primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
                                                                                                                                                                                                          AW010330 605 bp mRNA linear EST 10-SE ST04G06 Fine Triplex shoot tip library Plnus taeda cDNA clone ST04G06, mRNA sequence.
                                                                                                                                                                    loblolly pine.
Pinus taeda
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organism="Pinus taeda"
/db_xref="taxon:3352"
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AL568166 AL568166
BI416777 hasp002xd
BH422732 BOGRM52TF
BH444988 BOGYABOTR
BE981479 UI-M-CG0p
BE981840 UI-M-CG0p
BE981890 UI-M-CG0p
BE981926 UI-M-CG0p
BE981926 UI-M-CG0p

C82886 C82886

EST 10-SEP-1999

BN160808 EST563342
AW357904 687063G11
BM160535 EST563058
B1473509 fp38b10.y
BM163034 EST565557
AQ751030 HS 5576 B
BH721895 BOHWT13TR
A2458762 1M0265F07
BE051991 GA E8001
BG136361 EST476803
BM359106 GA E8001
AL407572 T7 end of
A2012832 RPCI-23-3
BG733428 37131 MA
AZ248820 RPCI-23-9
AW334443 S34H9 AGS

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          /(lone_lib="Pine_TriplEx shoot tip library"
//lab_host="E. coli BM25.8"
//lab_host="E. coli BM25.8"
//note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
Sfil (A), Site_2: Sfil (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRAN isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in B. coli strain BM25.8 and sequenced from the 5' end."
sequenced from the 5' end."
9 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 15-AUG-2001
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subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
annosum cDNA clone hasp001xd12f, mRNA sequence.
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/db xref="taxon:169015"
/clone="hasp001xd12f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.
                                                                                                                                                                                                                                                                                                                                                Score 88.8; DB 10; Length 605;
Pred. No. 1.3e-14;
0; Mismatches 97; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Pinus sylvestris/Heterobasidion annosum
Eukaryota, mixed EST libraries.
1 (bases 1 to 726)
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Email: FracA.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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'clone="ST04G06"
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Fax: +46 18 30 92 45
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/db_xxef="rexnorms 15015"
/clone="hasp002xp15f"
/clone="hasp002xp15f"
/clone=lib="heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
/dev_stage="Seedling roots of scots pine were infected for
/dev_stage="Seedling roots of scots pine were infected for
/note="Wetcor: pT-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
plue roots infected for 6-days with mycelia of
plue roots infected for 8-days with mycelia of
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Eukaryota, mixed EST libraries.

I (bases 1 to 750)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Hererobasidion annosum) with unpublished (2001)
6 days with H. annosum."
//note="Vector: pT-Adv. Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pher rocts infected for 6-days with mycelia of Heterobassidon annosum (FPS)."
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Pinus sylvestris/Heterobasidion annosum"
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Pred. No. 1.4e-14;
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Tex: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seg primer: T7 primer.
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                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGCCAGACTGCTTCTGCTTACAACACGGCCAACTGCAAAGGCGTTGCTCAGACCGGTT 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGGTCCAGTGCCA---GGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAAT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW043287 598 bp mRNA linear ST31E09 Pine TriplEx shoot tip library Pinus taeda ST31E09, mRNA sequence.
AW043287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
,NC, 27695-8008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R. The Pine Gene Discovery Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus taeda
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                      Similarity
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                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              919-515-7800
919-515-7801
    Conservative
                                                                                                                                                                /clone lib="Pine TriplEx shoot tip library"
/clone lib="Pine TriplEx shoot tip library"
/lab host="E. coli BM25.8"
/note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
/note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
Sfil (A); Site_2: Sfil (B); Shoot tips (approx. 2 cm from sell) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were
                                                                                                     recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
3 126 c 150 g 171 t 5 others
                                                                                                                                                                                                                                                                                                                                                                   /organism="Pinus taeda"
/db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                               /clone="ST31E09"
                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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                    17.4%;
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Pred. No. 9.2e-14;
    0
                      Score 85.6; DB 10;
Pred. No. 1.1e-13;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing
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                                           Length 598;
         Indels
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      9;
         Gaps
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                                                                                                           Query Match
Best Local
                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 CTGGACAAACTGCTGCTCTCTACAACCAGGCTGGTGCAGGTGCTGCTGCACACACCAGGT 316
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144 AGGGCAGTTATTTCACTGCGTGGGCAGGGCCTGGTTGTAACAACCATGCTGCGCGATACA 203
                                         143 ATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATA 202
                                                                                                           Local Similarity
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                                                                                       159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 698)
Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
Expressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hasp002xj10f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xj10f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pinus sylvestris/Heterobasidion annosum pinus sylvestris/Heterobasidion annosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,8-750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI416872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +46 18 67 15 98 Fax: +46 18 30 92 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Fred.Asiegbu@mykopat.slu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sweden
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                                                                                         Conservative
                                                                                                                                                                                                                /dev_stages"Seedling roots of scots pine were infected for 6 days with H. annosum"

/notes"Vector: PT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycella of Heterobasidon annosum (FPS)."
                                                                                                                                                                                                                                                                                                                                                 /clone="hasp002xj10f"
/clone lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
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                                                                                                              17.2%;
                                                                                         0; Mismatches
                                                                                                                Score 85; DB 13;
Pred. No. 1.7e-13;
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203 GCAAGTGTGGATGCTCAGCTATACATCAGAAG-----GGAGGCTATGACTTCAGCTACA 256

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374 GCTA 377
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                                                                                                                                                                                                                                                                                                              hasp001xh23f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp001xh23f, mRNA sequence.
204 GCAAATGTGGGTGTTCTAATGGGCAACATTCATGGAGGATACGAGTTCATGTATC 263
                                                                               264 AAGGCCÁGGÁCGCTTGCGGCTTACAACACGGACAACTGCAAGGGCGTTGCTCAGACCCGGT 323
                                                                                                               TIGGGICCAGIGCCA---GGGCAIGCAACCCITITIGGITGGAAGAGIAICTICAICCAAI 373
                                                                                                                                            324 TITCTAGCAGIGITAATCAAGCTIGCAGCAGITITIGGITGGAAGAGTITITITCATCAGT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AGGCAGTTATTTCACTGCGTGGGCAGGCCTGGTTGCAACAACCATGCTGCTCGATACA 200
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/db_xref="taxon:169015"
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                                                                                                                                                                                                                                                                                                     linear
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Eukaryota, mixed EST libraries.
1 (bases 1 to 531)
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Fax: +46 18 30 92 45
Email: Fred Aslegbu@mykopat.slu.se
                                                                                                                                                                                                                                                                                                    531 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7 primer.
Location/Qualifiers
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TITLE
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BI416595
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/organism="Pinus sylvestris/Heterobasidion annosum"
/db xref="taxon:169015"
/clone="haspootxd04f"
/clone="haspootxd04f"
/clone=haspootxd04f"
/clone=haspootxd04f"
/clone=haspootxd04f"
/dev_stage="Seedling roots of scots pine were infection stage subtraction cDNA library (hasp)"
/dev_stage="Seedling roots of scots pine were infected for fore="Vector: pT-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
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                                             317 TIGGGTCCAGTGCCA---GGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAAT 373
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
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Fax: +46 18 30 92 45
Email: Fred. Asiagbuomykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
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                                                                      GCTA 304
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer:
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/clone lib="Heterobasidion annosum - Scots pine infection stage Bubtraction cDNA library (hasp)"
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/db_xref="taxon:169015"
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                                    BI416868 530 bp mRNA linear EST 15-AUG-2001 hasp002xj06f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xj06f, mRNA sequence.
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.
Seq primer: T7 primer.
Seq primer: T7 primer.
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Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
Expressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
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hasp002x103f Heterobasidion annosum - Scots pine infection stag
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annosum cDNA clone hasp002x103f, mRNA sequence.
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Dept. of Forest Mycology & Pathology
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6 days with H. annosum"
7 note="Vector: pT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
8 146 C 177 g 227 t 6 others
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/dev stage="%seAlir rollibrary"
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/clone="hasp002x103f"
/clone_lib="Heterobasidion annosum -
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/clone=lhasp002xj06f"
/clone=lb="Heterobasidion annosum - Scots pine infection stage subtraction CDNA library (hasp)"
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/note="Vector: PT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
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                Pinus sylvestris/Heterobasidion annosum.

Pinus sylvestris/Heterobasidion annosum
Eukaryote; mixed EST libraries.

1 (bases 1 to 530)

Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.

Bypressed sequence tags of randomly selected cDNA clones from the seedling roots of Scots pine (Funus sylvestris)

Unpublished (2001)

Contact: Fred O. Asiegbu
Dept. of Rorest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 GCAAGTGTGGATGCTCAGCTATACATCAGAAG-----GGAGGCTATGACTTCAGCTACA 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
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Pinus sylvestris/Hererobasidion annosum
Eukaryota; mixed EST libraries.
1 (bases 1 to 697)
                                                                                                                                                                                                                                                                                                                    Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbuemykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
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/clone="hasp001xn07f"
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/clone lib="Heterobasidion annosum - Scots pine infection
/clone lib="Heterobasidion con library (hasp)"
/clove stage="Seedling roots of scots pine were infected for
/clote="Vector: pT-Adv; Site 1: EcoRI; The subtractive
/chote="Vector: pT-Adv; Site 1: EcoRI; The subtractive
/chote="Vector: pT-Adv; Site 2: EcoRI; The subtractive
/clote="Vector: pT-Adv; Site 2: EcoRI; T
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Bi416665

Bibp mRNA linear EST 15-AUG-2001
hasp001xn05f Heterobasidion annosum - Scots pine infection stage
subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
annosum cDNA clone hasp01xn05f, mRNA sequence.
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Pinus sylvestris/Heterobasidion annosum
Eukaryota, mixed EST libraries.

1 (bases 1 to 531)

Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.

Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with Unpublished (2001)

Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                     Unpublished (2001)
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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/db_xref="taxon:169015"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbuomykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
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                                                                                                                                                                                               Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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Email: Fred.Asiegbu@mykopat.slu.
Seq primer: T7 primer
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Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
                                                                                                               Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750
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6 days with H. annosum"
6 days with H. annosum"
7 note="Vector: pT-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scote pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)."
8 118 c 138 g 158 t
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/dev_stage="Seedling roots of scots pine were infected for
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1. No. 2e-12;
1. no. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACAAACTGCTGCTCTACAACCAGGCTGGATGCAGTGGTGTTGCACACACCAGGT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAAGTGTGGATGCTCAGCTATACATCAGAAG-----GGAGGCTATGACTTCAGCTACA 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGGTCCAGTGCCA---GGGCATGCAACCCTTTTGGTTGGAAGAGTAT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hasp001xf17f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp001xf17f, mRNA sequence.
                                                                                                                                                                                                                Tal: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbudmykopat.slu.se
Seq primer: T7 primer.
                                                                                                                                                                                                                                                                                                                             Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, B
                                                                                                                                                                                                                                                                                                                                                                                                               Pinus sylvestris/Heterobasidion annosum
Eukaryota; mixed EST libraries.

1 (bases 1 to 476)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from
interaction of the root rot fungus (Heterobasidion annosum) wi
seedling roots of Scots pine (Pinus sylvestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI416558
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                                                                                                                                                                                                                                                                                                              Sweden
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/dev_stage="Seedling roots of scots pine were infected foays with H. annosum"
/note="Vector: pT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
                    stage Subtraction cDNA library (hasp)
/dev_stage="Seedling roots of scots p
6 days with H. annosum"
                                                                               /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
/clone="hasp001xf17f"
/clone_11b="Heterobasidion annosum - Scots pine inf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="hasp002xa22f"
/clone_lib="Heterobasidion annosum -
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/db_xref="taxon:169015"
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/note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
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Pred. No. 6.2e-11;
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                                                                          Scots pine infection
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                                             were infected for
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/organism="Pinus taeda"
/db xref="taxon:3152"
/clone="8762/8762406"
/clone="8762/8762406"
/clone="8762/8762406"
/clone="8762/8762406"
/clone="8762/8762406"
/clone="8762/8762406"
/lab_host="E. coli BM25.8"
/note="0rgan: shoot tips; Vector: Lambda TriplEx; Site_1: Sfil (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SNART-PCR method (clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector: Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

10 a 67 c 69 g 77 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 bp mRNA linear EST 08-SEP-2000 ST62/ST62H06 Pine TriplEx shoot tip library Pinus taeda cDNA clone ST65/ST62H06, mRNA sequence.
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus,
1 (bases 1 to 294)
Metten, W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)." I others
                                                                                                                                                                                                                                                                                                      452 ATGGAGGATACGAGTTCATGTATCAAGGCCAGACCGCTGCGGCTTACAACACGGACAACT 393
                                                                                                                                                                                                                                                                                                                                                             293 GCAGTGGTGTTGCACACACACGTTTGGGTCCAGTGCCAGG---GCATGCAACCCTTTTG 349
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                                                                                                                                                                                                                                                         233 AGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGCTGGAT 292
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                                                                                                                                                                                                          ъ,
                                                                                                                                                   11.6%; Score 57.4; DB 13; Length 476; 66.7%; Pred. No. 1.3e-05; tive 0; Mismatches 46; Indels 3;
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Seg primer: 5' lambda TriplEx2 Seguencing Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGGAAGAGTTTTTTCATCCAGTGCT 306
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Tel: 919-515-7800
Fax: 919-515-7801
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Best Local Similarity
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BE662406
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Search completed: January 12, 2003, 08:35:41 Job time : 1953 secs